MARINE MAMMAL & TURTLE DIVISION (MMTD), PUBLICATIONS

Personnel from the Marine Mammal & Turtle Division are in "bold" PDF available upon request from authors

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Week of 21 September 2015

taxa.

Curtis, K. A., Moore, J. E., Benson, S. R. 2015. Estimating Limit Reference Points for Western Pacific Leatherback Turtles (*Dermochelys coriacea*) in the U. S. West Coast EEZ. PLoS ONE 10(9): e0136452. doi:10.1371/journal.pone.0136452 (http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0136452)

Abstract - Biological limit reference points (LRPs) for fisheries catch represent upper bounds that avoid undesirable population states. LRPs can support consistent management evaluation among species and regions, and can advance ecosystem-based fisheries management. For transboundary species, LRPs prorated by local abundance can inform local management decisions when international coordination is lacking. We estimated LRPs for western Pacific leatherbacks in the U.S. West Coast Exclusive Economic Zone (WCEEZ) using three approaches with different types of information on local abundance. For the current application, the bestinformed LRP used a local abundance estimate derived from nest counts, vital rate information, satellite tag data, and fishery observer data, and was calculated with a Potential Biological Removal estimator. Management strategy evaluation was used to set tuning parameters of the LRP estimators to satisfy risk tolerances for falling below population thresholds, and to evaluate sensitivity of population outcomes to bias in key inputs. We estimated local LRPs consistent with three hypothetical management objectives: allowing the population to rebuild to its maximum net productivity level (4.7 turtles per five years), limiting delay of population rebuilding (0.8 turtles per five years), or only preventing further decline (7.7 turtles per five years). These LRPs pertain to all human-caused removals and represent the WCEEZ contribution to meeting population management objectives within a broader international cooperative framework. We present multi-year estimates, because at low LRP values, annual assessments are prone to substantial error that can lead to volatile and costly

management without providing further conservation benefit. The novel approach and the performance criteria used here are not a direct expression of the "jeopardy" standard of the U.S. Endangered Species Act, but they provide useful assessment information and could help guide international management frameworks. Given the range of abundance data scenarios addressed, LRPs should be estimable for many other areas, populations, and

Report: Training Workshop to Develop Best Practices for Collecting Data to Estimate Marine Mammal Abundance on the Pacific Coast of South America, Salinas, Ecuador, August 2015. Available online at http://cpps.dyndns.info/cpps-docs-web/planaccion/docs2015/Curso MMarinos 2015/CPPS-
NOAA% 20Trainign% 20Salinas% 20report 11092015.pdf. Contact Jessica.Redfern@noaa.gov for details.

Summary - A training workshop on best practices to collect data to estimate marine mammal abundance on the Pacific coast of South America was carried out at Salinas, Ecuador, 18-20 August 2015. The activity was conducted in the framework of the cooperation between the USA National Oceanic and Atmospheric Administration (NOAA) and the Permanent Commission for the South Pacific and in implementing the Marine Mammal Action Plan for the Conservation of Marine Mammals in the Southeast Pacific. The lack of information on abundance and population trends for the vast majority of species inhabiting this area is a major gap that deserves attention.

The annual regional oceanographic cruises coordinated by CPPS in four countries (Chile, Colombia, Ecuador and Peru) have been identified as potential platforms for collecting data that can be used to estimate marine mammal abundance. However, large scale assessments require the use of standardized methodologies and expertise. Thus, the workshop objectives were to: 1) Provide training to marine mammal researchers in the region about best practices for collecting data that can be used to estimate abundance; 2) Promote research on marine mammals with a regional focus, standardizing monitoring techniques and data sharing; 3) Strengthen the bonds of cooperation with NOAA researchers with experience in marine mammal population assessments in the eastern Pacific; 4) Define the basic requirements for the creation of a regional long-term program to assess

marine mammal populations in the Southeast Pacific. The workshop was attended by 23 people from 5 countries and included representatives from governmental research institutions, universities, and NGO's. The current data collection practices in the four countries were reviewed. Regional expertise was shared about using line-transect methodology to estimate the abundance of river dolphins and baleen whales in coastal areas. Personnel from the SWFCS shared their expertise about data collection protocols used during their marine mammal and ecosystem assessment surveys in the Eastern tropical Pacific and on west coast of the USA. These procedures have been extensively used and tested. Numerous publications are available about these protocols. Participants also received information about the basics of line-transect sampling theory.

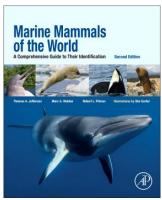
On the second day, participants had the opportunity to apply data collection protocols and use new equipment during five hours of field training on board a yacht rented for this purpose. Trainees filled out sightings and effort logs and estimated group sizes, distance to sightings, and angle to sightings.

On the final day of the workshop, participants discussed the field training and agreed on the best data collection procedures. Specifically, they reached agreement on equipment, data recording, observers and effort, protocols for sightings, estimating group size, passing and closing protocols, and topics for future workshops. Finally, participants made recommendations for CPPS, the individual countries, and researchers about the best procedures to collect data on future marine mammal surveys in the Southeast Pacific.

Week of 14 September 2015

Thomas A. Jefferson, Marc. A. Webber, and **Robert L. Pitman**. 2015. Marine Mammals of the World, 2nd Edition: *A Comprehensive Guide to Their Identification*. Academic Press. Pp. 616.

Description - This new edition of Marine Mammals of the World describes and illustrates newly discovered and rarely photographed species, making it the most comprehensive and up-to-date marine mammal identification guide available. This edition continues to meet the research-focused needs of marine biologists and conservation biologists by providing a tremendous influx of new photos, taking advantage of advances in digital and auto-focusing photography, and the emergence of marine mammal studies and "whalewatching" around the world. The book encompasses cetacean, pinniped, and sirenian species, as well as extinct species, and describes basic biology and taxonomic groupings of marine mammals.



Week of 7 September 2015

K. Alexandra Curtis, Jeffrey E. Moore, Charlotte Boyd, Peter W. Dillingham, Rebecca L. Lewison, Barbara L. Taylor, Kelsey C. James. 2015. Managing catch of marine megafauna: Guidelines for setting limit reference points, Marine Policy 61: 249-263. (http://www.sciencedirect.com/science/article/pii/S0308597X15002031)

Abstract - Limit reference points (LRPs) for catch, which correspond to thresholds to undesirable population or ecosystem states, offer a consistent, objective approach to management evaluation and prioritization across fisheries, species, and jurisdictions. LRPs have been applied successfully to manage catch of some marine megafauna (elasmobranchs, marine reptiles, seabirds, and marine mammals) in some jurisdictions, such as the use of Potential Biological Removal (PBR) to manage incidental mortality of marine mammals under the U.S. Marine Mammal Protection Act. However, implementation of ecosystem-based management is still in its infancy globally, and LRPs have not yet been widely adopted for marine megafauna, particularly for incidental catch. Here, guidelines are proposed for estimating catch LRPs for marine megafauna, with particular attention to resolving common technical and political challenges, including (1) identifying management units, population thresholds, and risk tolerances that align with common conservation goals and best practices, (2) choosing catch LRP estimators, (3) estimating input parameters such as abundance and productivity, (4) handling uncertainty, and (5) dealing with mismatches between management jurisdictions and population boundaries. The problem of cumulative impacts across sectors is briefly addressed. These guidelines, grounded in marine policy, science, precedent, and lessons learned, should facilitate wider application of catch LRPs in evaluation and management of fisheries impacts on marine megafauna, in support of global commitments to conserve biodiversity and manage fisheries responsibly.

Benjamin D. Charlton, **Jennifer L. Keating**, Li Rengui, Yan Huang, and Ronald R. Swaisgood. 2015. The acoustic structure of male giant panda bleats varies according to intersexual context. J. Acoust. Soc. Am. 138: 1305-1312. (http://dx.doi.org/10.1121/1.4928606)

Abstract - Although the acoustic structure of mammal vocal signals often varies according to the social context of emission, relatively few mammal studies have examined acoustic variation during intersexual advertisement. In the current study male giant panda bleats were recorded during the breeding season in three behavioural contexts: vocalising alone, during vocal interactions with females outside of peak oestrus, and during vocal interactions with peak-oestrous females. Male bleats produced during vocal interactions with peak-oestrous females were longer in duration and had higher mean fundamental frequency than those produced when males were either involved in a vocal interaction with a female outside of peak oestrus or vocalising alone. In addition, males produced bleats with higher rates of fundamental frequency modulation when they were vocalising alone than when they were interacting with females. These results show that acoustic features of male giant panda bleats have the potential to signal the caller's motivational state, and suggest that males increase the rate of fundamental frequency modulation in bleats when they are alone to maximally broadcast their quality and promote close-range contact with receptive females during the breeding season.

Week of 24 August 2015

Carretta, J. V., M. M. Muto, S. Wilkin, J. Greenman, K. Wilkinson, M. DeAngelis, J. Viezbicke, D. Lawson, J. Rusin, and J. Jannot. 2015. Sources of human-related injury and mortality for U.S. Pacific west coast marine mammal stock assessments, 2009-2013. U.S. Department of Commerce, NOAA Technical Memorandum, NOAA-TM-NMFS-SWFSC-548. 108 p. (https://swfsc.noaa.gov/publications/TM/SWFSC/NOAA-TM-NMFS-SWFSC-548.pdf)

Summary - The Marine Mammal Protection Act (MMPA) requires the National Oceanic and Atmospheric Administration (NOAA), National Marine Fisheries Service (NMFS), to document human-caused mortality, non-serious injury (NSI), and serious injury (SI) of marine mammals a part of assessing marine mammal stocks and to evaluate human-caused injury and mortality levels in the context of potential biological removal (PBR) levels calculated under the MMPA (Wade 1998). NMFS defines SI as "any injury that will likely result in mortality." While documenting mortality is straightforward, distinguishing NSI from SI requires reliable data on injury severity and animal condition, often in challenging environments where thorough examination of injuries is not possible. NMFS updated its SI designation and reporting process in 2012, using guidance from previous workshops (Angliss and DeMaster 1998, Andersen et al. 2008), expert opinion, and analysis of historic injury cases to develop new criteria for distinguishing SI from NSI (NMFS 2012a, 2012b; NOAA 2012; Moore et al. 2013).

This report contains updated records of human-caused injury and mortality to pinnipeds and cetaceans from 2009 to 2013 for marine mammal populations that occur in U.S. west coast waters and which are evaluated in Pacific region marine mammal stock assessment reports (SARs) (Carretta et al. 2013a, 2013b). Mortality records, while included in this report, were obviously not evaluated for SI/NSI status. Subsistence and directed takes (i.e., gray whales taken by Russian natives) are not reported here but are reported in SARs published by NMFS. Previous records, including cases from 2007 and 2008, are published in previous reports (Carretta et al. 2013a, 2014).

Sources of injury data include strandings, disentanglement networks, and fishery observer programs. Stranding network data includes records of injured marine mammals at sea and ashore reported by the public, as well as researchers. Injury sources include, but are not limited to, vessel strikes, gillnet entanglement, pot and trap gear entanglement, shootings, marine debris entanglement, research-related injuries/deaths, hook and line fishery interactions, and power plant water intake entrainment. Most records originate from stranding networks in California, Oregon, and Washington, though a few Alaska records of Eastern North Pacific gray whales (*Eschrichtius robustus*) are included, because this population is assessed in the Pacific region SARs and occurs along the U.S. west coast. Other marine mammals, such as Steller sea lions (*Eumetopias jubatus*), occur in California, Oregon, and Washington waters, but they are assessed in Alaska region SARs (Allen and Angliss 2014) and are not included in this report. Injury determinations for Pacific region species/stocks in the central Pacific from Hawaii westward are also included in separate reports.

Carretta, J. V., E. M. Oleson, D. W. Weller, A. R. Lang, K. A. Forney, J. Baker, M. M. Muto, B. Hanson, A. J. Orr, H. Huber, M. S. Lowry, J. Barlow, J. E. Moore, D. Lynch, L. Carswell, and R. L. Brownell, Jr. 2015. U.S. Pacific Marine Mammal Stock Assessments: 2014. U.S. Department of Commerce, NOAA Technical Memorandum, NOAA-TMNMFS-SWFSC-549. 414 p. (https://swfsc.noaa.gov/publications/TM/SWFSC/NOAA-TM-NMFS-SWFSC-549.pdf - electronic copies only available.)

Summary - Under the 1994 amendments to the Marine Mammal Protection Act (MMPA), the National Marine Fisheries Service (NMFS) and the U.S. Fish and Wildlife Service (USFWS) are required to publish Stock Assessment Reports for all stocks of marine mammals within U.S. waters, to review new information every year for strategic stocks and every three years for non-strategic stocks, and to update the stock assessment reports when significant new information becomes available.

Pacific region stock assessments include those studied by the Southwest Fisheries Science Center (SWFSC, La Jolla, CA), the Pacific Islands Fisheries Science Center (PIFSC, Honolulu, HI), the National Marine Mammal Laboratory (NMML, Seattle, WA), and the Northwest Fisheries Science Center (NWFSC, Seattle, WA).

The 2014 Pacific marine mammal stock assessments include revised reports for 11 Pacific marine mammal stocks under NMFS jurisdiction, including six "strategic" stocks: Hawaiian monk seal, Southern Resident killer whale, Main Hawaiian Islands Insular false killer whale, Hawaii Pelagic false killer whale, California/Oregon/Washington sperm whale, and Western North Pacific gray whale. New abundance estimates are available for three stocks in the Pacific Islands region and five U.S. west coast stocks. New estimates of abundance for the California/Oregon/Washington stock of sperm whales are based on a Bayesian trend analysis that utilizes previously collected line-transect data (Moore and Barlow, 2014), resulting in a more stable time series of abundance estimates. Mortality and serious injury estimates of California/Oregon/Washington sperm whales in California drift gillnets are updated, based on pooling additional years of data (>5 years) to reduce bias and improve precision in mean annual bycatch estimates (Carretta and Moore 2014). The combination of new abundance estimates and pooling of bycatch estimates over a longer time period for this stock of sperm whales results in mean annual bycatch estimates that no longer exceed PBR. In addition, a new stock assessment report for Western North Pacific gray whales is presented for the first time, prompted by new data showing that gray whales previously photographed in the western North Pacific utilize U.S. and Mexican waters.

Week of 3 August 2015

Durban, J. W., Fearnbach, H., Barrett-Lennard, L. G., **Perryman, W. L.**, and LeRoi, D. J. 2015. Photogrammetry of killer whales using a small hexacopter launched at sea. Journal of Unmanned Vehicle Systems, Published online 30 June 2015, 10.1139/juvs-2015-0020. (http://www.nrcresearchpress.com/doi/pdf/10.1139/juvs-2015-0020)

Abstract - Conventional aircraft have been used for photogrammetry studies of free ranging whales, but are often not practical in remote regions or not affordable. Here we report on the use of a small, unmanned hexacopter (APH-22; Aerial Imaging Solutions) as an alternative method for collecting photographs to measure killer whales (*Orcinus orca*) at sea. We deployed and retrieved the hexacopter by hand during 60 flights (average duration 13.2 min, max 15.7 min) from the upper deck of an 8.2 m boat, utilizing the aircraft's vertical takeoff and landing (VTOL) capability. The hexacopter was quiet and stable in flight, and therefore could be flown at relatively low altitudes without disturbing whales. The payload was a Micro Four-Thirds system camera that was used to obtain 18920 still images from an altitude of 35–40 m above the whales. Tests indicated a ground-resolved distance of <1.4 cm across the full extent of a flat and undistorted field of view, and an onboard pressure altimeter enabled measurements in pixels to be scaled to true size with an average accuracy of 5 cm. As a result, the images were sharp enough to differentiate individual whales using natural markings (77 whales in total) and preliminary estimates resolved differences in whale lengths ranging from 2.6 to 5.8 m. This first application at sea demonstrated the APH-22 hexacopter to be a safe and cost-effective platform for collecting photogrammetry images to fill key scientific data gaps about whales, and we anticipate this utility will extend to studies of other wildlife species.

Sampson, L., Giraldo, A., Payán, L. F., Amorocho, D. F., **Eguchi T.**, **Seminoff J. A.** (2015) Somatic growth of juvenile green turtle (Chelonia mydas) morphotypes in the Colombian Pacific. Marine Biology doi:10.1007/s00227-015-2692-y.

Abstract - Somatic growth rates of green turtles (*Chelonia mydas*) are affected by foraging success and influence their survival and reproduction. Gorgona National Park (GNP) in the Colombian Pacific ($2^{\circ}58'03''$ N, $78^{\circ}10'49''$ W) is an insular foraging site that offers a unique opportunity to study the black (occurring only in the eastern Pacific) and yellow (with western Pacific nesting beach origins) morphotypes of green turtles during their juvenile phase. A total of 995 turtles were captured and marked between October 2003 and December 2012. Recapture rates were low (20 black morphotype and 13 yellow morphotype turtles) but suggested that at least some turtles remain in the area for extended periods (>5 years). Mean growth rate was slightly higher for black morphotype (mean 0.92 ± 0.24 cm/y) than yellow morphotype turtles (mean 0.74 ± 0.26 cm/y), and both morphotypes displayed a non-monotonic growth pattern. Black morphotype turtles grew faster at intermediate sizes, similar to black turtles at other locations in the eastern Pacific, whereas yellow morphotype turtles had slowest growth at intermediate sizes. Our data underscore the importance of GNP as a foraging habitat for C. mydas individuals from distinct nesting populations and indicate that these morphotypes have different growth patterns while residing at the same foraging site.

Morin, P. A., Parsons, K. M., Archer, F. I., Ávila-Arcos, M. C., Barrett-Lennard, L. G., Dalla Rosa, L., Duchêne, S., Durban, J. W., Ellis, G., Ferguson, S. H., Ford, J. K., Ford, M., Garilao, C., Gilbert, M. T. P., Kaschner, K., Matkin, C. O., Petersen, S. D., Robertson, K. M., Visser, I. N., Wade, P. R., Ho, S. Y. W., Foote, A. D., 2015. Geographic and temporal dynamics of a global radiation and diversification in the killer whale. Molecular Ecology 24: 3964-3979. Abstract - Global climate change during the Late Pleistocene periodically encroached and then released habitat during the glacial cycles, causing range expansions and contractions in some species. These dynamics have played a major role in geographic radiations, diversification and speciation. We investigate these dynamics in the most widely distributed of marine mammals, the killer whale (Orcinus orca), using a global data set of over 450 samples. This marine top predator inhabits coastal and pelagic ecosystems ranging from the ice edge to the tropics, often exhibiting ecological, behavioural and morphological variation suggestive of local adaptation accompanied by reproductive isolation. Results suggest a rapid global radiation occurred over the last 350 000 years. Based on habitat models, we estimated there was only a 15% global contraction of core suitable habitat during the last glacial maximum, and the resources appeared to sustain a constant global effective female population size throughout the Late Pleistocene. Reconstruction of the ancestral phylogeography highlighted the high mobility of this species, identifying 22 strongly supported long-range dispersal events including interoceanic and interhemispheric movement. Despite this propensity for geographic dispersal, the increased sampling of this study uncovered very few potential examples of ancestral dispersal among ecotypes. Concordance of nuclear and mitochondrial data further confirms genetic cohesiveness, with little or no current gene flow among sympatric ecotypes. Taken as a whole, our data suggest that the glacial cycles influenced local populations in different ways, with no clear global pattern, but with secondary contact among lineages

Week of 20 July 2015

Defran, R. H., M. Caldwell, E. Morteo, A. R. Lang, M. G. Rice, and D. W. Weller. 2015. Possible stock structure of coastal bottlenose dolphins off Baja California and California revealed by photo-identification research. Bulletin of the Southern California Academy of Sciences 114:1-11.

following long-range dispersal as a potential mechanism driving ecological diversification.

Abstract - Boat-based photo-identification research has been carried out on bottlenose dolphins in eastern North Pacific coastal waters off northern Baja California, Mexico and southern and central California, USA from 1981 to 2001. Within these waters, bottlenose dolphins routinely travel back and forth between coastal locations while generally staying within a narrow corridor extending only 1–2 km from the shore. Inter-area match rates for 616 dolphins photo-identified between 1981–2000 in four California coastal study areas (CCSAs) of Ensenada, San Diego, Orange County and Santa Barbara averaged 76%. To explore possible southern range limits for these dolphins, photo-identification surveys were carried out in the coastal waters off San Quintín, Baja California, Mexico between April-August 1990 (n=8 surveys) and July 1999 to June 2000 (n=12 surveys). The 207 individual dolphins identified off San Quintín were compared to the 616 dolphins identified in the CCSAs. The inter-area match rate between San Quintín and the CCSAs was 3.4% (n=7 dolphins). This low rate contrasts sharply with the much higher average match rate of 76% observed between the CCSAs. These differences in match rates suggest that both a California coastal stock and coastal Northern Baja California stock may exist, with only a limited degree of mixing between them.

Peschko, V., Ronnenberg, K, Siebert, U., and **Gilles, A.** 2016. Trends of harbour porpoise (*Phocoena phocoena*) density in the southern North Sea. Ecological Indicators 60: 174-183, DOI 10.1016/j.ecolind.2015.06.030

Abstract - In the southern North Sea, harbour porpoise occurrence increased in recent years after a phase of low abundances during earlier decades. Only very few studies on porpoise presence in the southern German North Sea exist so far. As anthropogenic activities will strongly increase in this part of the North Sea during the next years it is most important to assess population level effects. This study focuses on the analysis of temporal and spatial trends in porpoise density in this area of recent change. Dedicated aerial line-transect distance sampling surveys were conducted in the southern German North Sea between May 2002 and June 2013 to assess porpoise density and distribution. Statistical inferences on porpoise population trends were made using a Markov Chain Monte Carlo (MCMC) technique. Two approaches were chosen to test for a trend in porpoise density and an additional model focused on the change in density of calves. During 55,820 km of survey effort 4377 porpoises including 140 calves were recorded. A significant effect of increasing spatial aggregation from the lower density areas in the south-eastern German Bight to hot spot areas in the western parts was detected. For the western part of the study area a significant increase in porpoise density between 2002 and 2013 was detected. Seasons were significantly different with highest porpoise density in spring and successively decreasing densities in summer and autumn. From 2008 onwards high densities were also observed in summer. Calf density increased during the study period and was significantly higher in the west. On the basis of this extensive and unique dataset on porpoise occurrence in the southern German North Sea the findings clearly show that especially the south-western German North Sea serves as habitat of increasing importance for porpoises throughout the last decade. Definite reasons still remain unresolved. Changes in prey abundance or less favourable conditions in other areas could be important factors, which may also have caused a southward shift from high density areas in northern waters. On this baseline, further integrative approaches might lead to a sound understanding of the effect of anthropogenic activities on the future development of porpoise populations.

NMFS. 2015. Our living oceans: habitat. Status of the habitat of U.S. living marine resources. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-F/SPO-75, 327 p. doi: 10.7755/TMSPO.75.

NOAA NMFS SWFSC contributors: **Scott Benson**, John Butler, Paul Crone, **Peter Dutton**, **Karin Forney**, Kevin Hill, Suzanne Kohin, Alec MacCall, Franklin Schwing, Paul Smith, Susan Smith, Brian Spence, Kevin Stierhoff, and Xuemei Qiu. (MMTD contributors in bold)

Summary - Our Living Oceans habitat report provides a comprehensive summary of habitat information for all fishery and protected species under the purview of NOAA's National Marine Fisheries Service. The report provides information on habitat science, trends, and research needs nationally and on a region-specific basis. The report also provides a conceptual framework for understanding habitat-use patterns of marine species. It also identifies gaps in the available data and information, and describes how these gaps can be addressed through additional research. As with previous reports in the Our Living Oceans series, this publication and the data presented are the result of the collective efforts of National Marine Fisheries Service staff from around the country.

Week of 13 July 2015

Henderson, E. Elizabeth, **Karin A. Forney**, **Jay P. Barlow**, John A. Hildebrand, Annie B. Douglas, John Calambokidis, and William J. Sydeman. 2014. Effects of fluctuations in sea-surface temperature on the occurrence of small cetaceans off Southern California. Fishery Bulletin 112: 159-177.

Abstract - The link between ocean temperature and spatial and temporal distribution patterns of 8 species of small cetaceans off Southern California was examined during the period 1979–2009. Averages and anomalies of sea-surface temperatures (SSTs) were used as proxies for SST fluctuations on 3 temporal scales: seasonal, El Niño–Southern Oscillations (ENSO), and Pacific Decadal Oscillations (PDO). The hypothesis that cetacean species assemblages and habitat associations in southern California waters co-vary with these periodic changes in SST was tested by using generalized additive models. Seasonal SST averages were included as a predictor in the models for Dall's porpoise (Phocoenoides dalli), and common dolphins (Delphinus spp.), northern right whale dolphin (Lissodelphis borealis), and Risso's dolphin (Grampus griseus). The ENSO index was included as a predictor for northern right whale, long-beaked common (Delphinus capensis), and Risso's dolphins. The

PDO index was selected as a predictor for Dall's porpoise and Pacific white-sided (Lagenorhynchus obliquidens), common, and bottlenose (Tursiops truncatus) dolphins. A metric of bathymetric depth was included in every model, and seafloor slope was included in 5 of the 9 models, an indication of a distinctive spatial distribution for each species that may represent niche or resource partitioning in a region where multiple species have overlapping ranges. Temporal changes in distribution are likely a response to changes in prey abundance or dispersion, and these patterns associated with SST variation may foreshadow future, more permanent shifts in distribution range that are due to global climate change.

Week of 29 June 2015

Squires, D., **L. T. Ballance**, R. Deriso, J. Ianelli, M. Maunder, and K. Schaefer. 2015. Comment on 'Scope and compatibility of measures in international fisheries agreements' by Finus and Schneider. Oxford Economic Papers doi: 10.1093/oep/gpv041.

No abstract.

Chivers, S. J., W. L. Perryman, M. S. Lynn, T. Gerrodette, F. I. Archer, K. Danil, M. Berman-Kowalewski, and J. P. Dines. 2015. Comparison of reproductive parameters for populations of eastern North Pacific common dolphins: *Delphinus capensis* and *D. delphis*. Marine Mammal Science DOI: 10.1111/mms.12244. http://onlinelibrary.wiley.com/journal/10.1111/(ISSN)1748-7692/earlyview

Abstract - Reproductive parameters were estimated and compared for eastern North Pacific populations of common dolphins using specimen and photogrammetric data. Age and length data for *Delphinus capensis* and *D. delphis* specimens recovered as bycatch or strandings were used to estimate the postnatal growth rates needed to estimate age for calves measured in aerial photographs. Bayesian methods propagated uncertainty among models and revealed that the 2009 cohort of calves had birth dates centered on 6 March 2009 for *D. capensis* and 12 December 2008 for *D. delphis*. The evidence for discrete calving seasons suggests a mechanism of reproductive isolation has evolved between species. Photogrammetric data and Bayesian methods were also used to estimate the average length at which calves swim independently: 145.1 cm (\approx 11.1 mo) in *D. capensis* and 140.1 cm (\approx 14.0 mo) in *D. delphis*, and the proportion of calves (calves/dolphins counted): 0.045 in *D. capensis* and 0.069 in *D. delphis*. The latter parameter was converted to an index of calf production (calf/female dolphin) that was >50% lower than pregnancy rates suggesting few births occurred during the study year. Comparisons of regional differences in calf production suggest variability in habitat use patterns within the study area.

Week of 22 June 2015

Feist, Blake E., Marlene A. Bellman, **Elizabeth A. Becker, Karin A. Forney**, Michael J. Ford, and Phillip S. Levin. 2015. Potential overlap between cetaceans and commercial groundfish fleets that operate in the California Current Large Marine Ecosystem. NOAA Professional Paper NMFS 17, 27 p. doi:10.7755/PP.17

Abstract – Cetacean populations are confronted by many anthropogenic threats, including commercial whaling, noise, vessel collisions, gear entanglement, exploitative competition, habitat disturbance, and global climate change. Evidence indicates that commercial fishing activities can have both direct (e.g., gear entanglement and bycatch) and indirect (e.g., prey reduction and noise) effects on cetaceans. However, few studies have addressed the potential vulnerability of a given cetacean species to an entire fishing fleet that operates over a large marine ecosystem. In this study, we overlaid spatially explicit multiyear predicted mean densities of 11 cetacean species and 1 species guild within the California Current Large Marine Ecosystem with data for commercial fishing effort of the fixed-gear, at-sea hake mid-water trawl, and bottom trawl fleets of the west coast groundfish fishery. We quantified the exposure of each species to each fleet type by multiplying the predicted mean cetacean density by the measured fishing fleet effort. We found large interspecific and interfleet variability in the overlap between cetaceans and fishing fleets. Although many of the species had relatively low overlap rates, others had substantial exposure to some of the fishing fleets, particularly those species with more nearshore distributions. Direct mortality from these fleets has been documented to be low, but our results indicate that there is opportunity for fisheries interactions with some cetacean species, particularly in the fixedgear fleet. Our analyses make up an important first step in generating formal risk assessments for quantification of the impacts of various fishing fleets on populations of cetacean species that occur in the California Current.

Keen, E. 2015. Net savvy: A practical guide to zooplankton sampler design. NOAA Technical Memorandum NMFS-SWFSC-545.

Abstract - Plankton nets are widely used to sample phytoplankton, zooplankton and small nektonic animals. Here I present a step-by-step guide to designing plankton nets that fit the objectives of a study, the logistics of sampling, and the available budget. The primary three key parameters to determine in net design are mesh size, mouth diameter, and overall net length. These "key three" are related by the Open-Area Ratio (OAR), the ratio of effective filtering area to mouth area, which can be used to optimize sustained filtration performance for a target tow volume. Mesh size is determined first, which provides the expected porosity of the net and is primarily based on the smallest retained plankton size. Mouth size is then constrained according to avoidance capabilities of the target organisms and operational logistics. Overall net length is then set to achieve a target tow volume by meeting the minimum required OAR. All three factors can affect cost. Using this process, an array of potential net configurations can be evaluated. A case study is used to demonstrate this design process.

Week of 15 June 2015

Liles MJ, Peterson MJ, **Seminoff JA**, Altamirano E, Henríquez AV, **Gaos AR**, Gadea V, Urteaga J, Torres P, Wallace BP, Peterson TR. 2015. One size does not fit all: Importance of adjusting conservation practices for endangered hawksbill turtles to address local nesting habitat needs in the eastern Pacific Ocean. Biological Conservation 184:405–413.

Abstract - Conservation biologists frequently use data from the same or related species collected in diverse geographic locations to guide interventions in situations where its applicability is uncertain. There are dangers inherent to this approach. The nesting habitats of critically endangered hawksbill sea turtles (Eretmochelys *imbricat*a) cover a broad geographic global range. Based on data collected in the Caribbean and Indo-Pacific. conservationists assume hawksbills prefer open-coast beaches near coral reefs for nesting, and that individual hawksbills are highly consistent in nest placement, suggesting genetic factors partially account for variation in nest-site choice. We characterized nest-site preferences of hawksbills in El Salvador and Nicaragua, where >80% of nesting activity occurs for this species in the eastern Pacific, and >90% of hawksbill clutches are relocated to hatcheries for protection. We found hawksbills preferred nest sites with abundant vegetation on dynamic beaches within mangrove estuaries. Nests in El Salvador were located closer to the ocean and to the woody vegetation border than nests in Nicaragua, suggesting female hawksbills exhibit local adaptations to differences in nesting habitat. Individual hawksbills consistently placed nests under high percentages of overstory vegetation, but were not consistent in nest placement related to woody vegetation borders. We suggest conservation biologists use caution when generalizing about endangered species that invest in specific life-history strategies (e.g., nesting) over broad ranges based on data collected in distant locations when addressing conservation issues.

Fuentes MMPB, Bell I, Hagihara R, Hamann M, Hazel J, Huth A, **Seminoff JA**, Sobtzick S, Marsh H. 2015. Improving in-water estimates of marine turtle abundance by adjusting aerial survey counts for perception and availability biases. Journal of Experimental Marine Biology and Ecology 471:77–83

Abstract - Aerial surveys are often used to estimate wildlife abundance. The probability of detecting an animal during a survey involves two processes: (1) availability bias when animals present in the search area are not available for detection and (2) perception bias, when some animals potentially visible to observers are missed. Estimating these two sources of bias can lead to improved abundance estimates. However, to date, no marine turtle aerial survey has quantified both biases. To improve in-water marine turtle abundance estimates from aerial counts we estimated: (1) perception bias using independent tandem observers and mark recapture models, and (2) availability bias by quantifying the effect of turtle diving behaviour and environmental conditions on the detection probability of turtles. We compared unadjusted and adjusted abundance estimates to evaluate the effects of these detection biases in aerial surveys. Adjusted data produced a substantially higher estimate of turtles than the unadjusted data. Adjusting for availability bias increased the estimates 18.7 times; adjusting for perception bias resulted in a further 5% increase. These results emphasize the need to consider availability and perception corrections to obtain robust abundance estimates. This approach has application for aerial surveys for other marine wildlife including marine mammals and large sharks.

Week of 8 June 2015

Emily T. Griffiths, J. Scott Ferguson, Erin M. Oleson, and **Shannon Rankin**. 2015. Multi-bank Power Supply System for Small Towed Hydrophone Arrays. U.S. Dep. Commer., NOAA Tech. Memo. NOAA-TM-NMFS-SWFSC-544 (https://swfsc.noaa.gov/publications/TM/SWFSC/NOAA-TM-NMFS-SWFSC-544.pdf).

Abstract - Passive acoustic monitoring is quickly becoming a standard component of shipboard cetacean population surveys. Power supplies on survey vessels are often electronically noisy and result in poor quality recordings. An independent battery-powered voltage supply is regularly necessary for high quality recordings. Here we describe the design of a simple system to provide independent, single-sided 12 V power for a towed hydrophone system, such as the Southwest Fisheries Science Center's (SWFSC) Acoustic Recording System (ARS, Rankin et al. 2011) and hydrophone arrays. This system allows for simultaneous use of one battery bank while charging a depleted battery bank. This multi-battery bank system was successfully field tested by SWFSC for four and a half months during the 2014 California Current Cetacean and Ecosystem Assessment Survey (CalCurCEAS), and is based upon an original design Pacific Islands Fisheries Science Center (PIFSC) has been using since 2011.

Week of 1 June 2015

Loggerhead MSRA Technical Advisory Team (**Eguchi, T.**, Fahy, T., Kelly, I., **Seminoff, J.**, Swimmer, Y., and Wang, J.) 2015. Comparability evaluation for United States and Mexico fisheries that interact with North Pacific loggerhead sea turtles. NOAA Fisheries Technical Report. 101 pp.

Abstract - In July 2012, a mass-stranding of loggerhead sea turtles (Caretta caretta) along the Pacific coast of Baja California, Mexico, coupled with a report of significant bycatch in the gillnet fishery of Baja California Sur, prompted the National Marine Fisheries Service (NMFS), in January 2013, to formally identify Mexico for its lack of an effective regulatory program to end or reduce North Pacific loggerhead turtle bycatch in the gillnet fishery operating in the Gulf of Ulloa pursuant to the High Seas Driftnet Fishing Moratorium Protection Act (Moratorium Protection Act). As indicated in the statute, Mexico had two years to develop a regulatory program that would reduce or eliminate loggerhead turtle bycatch in the region comparable in effectiveness to the United States. In April 2015, Mexico provided the United States with its regulatory measures, which included the implementation of a 90-loggerhead turtle per season mortality cap, development of a spatially tiered reserve system in part of the area where loggerhead bycatch is known to occur, and establishment of an observer program with vessel monitoring and video surveillance system. This report presents a comparability analysis to assess if the management measures are "comparable to measures required in the United States," which is a requirement under the Moratorium Protection Act if a country is to be positively certified. NMFS will consider whether the program is comparable in effectiveness, taking into account different conditions that could bear on the feasibility and efficacy of comparable measures. Here we provide analyses of effectiveness based on several components of Mexico's regulatory framework, including an analysis of the maximum loggerhead mortalities per year in U.S. vs. Mexican fisheries that interact with North Pacific loggerhead turtles, spatial and temporal comparisons of time/area closures and restrictions, fisheries gear modifications, observer programs, and enforcement of regulations. We found that, while Mexico is to be commended on their development of new measures to reduce loggerhead bycatch - especially the 90 turtle mortality cap, there are several aspects of Mexico's regulations that are inconsistent with relevant ongoing management in U.S. fisheries. This Technical Report represents one element of a broader suite of considerations Agency leadership will use in their decision making to determine if Mexico's regulatory measures are comparable relative to the Moratorium Protection Act certification process for Mexico.

Week of 25 May 2015

Buoy Recorder (DASBR). U.S. Dep. Commer., NOAA Tech. Memo. NOAA-TM-NMFS-SWFSC-543. (https://swfsc.noaa.gov/publications/TM/SWFSC/NOAA-TM-NMFS-SWFSC-543.pdf)

Abstract - The Drifting Acoustic Spar Buoy Recorder (or DASBR) is an autonomous Passive Acoustic Monitoring (PAM) system developed at the Southwest Fisheries Science Center (SWFSC) to provide a practical, low-cost option for collecting high-quality marine acoustic data. Most autonomous recording systems (such as Cornell's Pop-ups and SIO's HARPS) are bottom mounted and therefore limited to shelf and slope waters. Fixed moorings in deep pelagic waters are generally too expensive for common use. Hydrophone arrays towed behind research vessels are often used to acoustically detect odontocetes in deeper waters, but they are not ideal. Ship time for towed array surveys is expensive, while ship and water flow noise prevent the collection of ambient noise data using towed arrays. Drifting recording units, such as DASBRs, are not limited to shallow waters, can record deep within the water column, and are isolated from ship noise and flow noise. Here we present the results of three DASBR field tests including two Passive Acoustic Sea Trials (PAST 2013 & PAST 2014) and the 2014 NOAA R/V Lasker shakedown mission trial. We discuss bioacoustic detections of marine mammals and alterations to the original design that were required to prepare the DASBRs for subsequent long-term deployments.

Week of 18 May 2015

Maxwell, S. M., E. L. Hazen, R. L. Lewison, D. C. Dunn, H. Bailey, S. J. Bograd, D. K. Briscoe, S. Fossette, A. J. Hobday, M. Bennett, S. Benson, M. R. Caldwell, D. P. Costa, H. Dewar, **T. Eguchi**, L. Hazen, S. Kohin, T. Sippel, and L. B. Crowder. 2015. Dynamic ocean management: Defining and conceptualizing real-time management of the ocean. Marine Policy 58 (2015) 42–50, http://dx.doi.org/10.1016/j.marpol.2015.03.014.

Abstract - Most spatial marine management techniques (e.g., marine protected areas) draw stationary boundaries around often mobile marine features, animals, or resource users. While these approaches can work for relatively stationary marine resources, to be most effective marine management must be as fluid in space and time as the resources and users we aim to manage. Instead, a shift towards dynamic ocean management is suggested, defined as management that rapidly changes in space and time in response to changes in the ocean and its users through the integration of near real-time biological, oceanographic, social and/or economic data. Dynamic management can refine the temporal and spatial scale of managed areas, thereby better balancing ecological and economic objectives. Temperature dependent habitat of a hypothetical mobile marine species was simulated to show the efficiency of dynamic management, finding that 82.0 to 34.2 percent less area needed to be managed using a dynamic approach. Dynamic management further complements existing management by increasing the speed at which decisions are implemented using predefined protocols. With advances in data collection and sharing, particularly in remote sensing, animal tracking, and mobile technology, managers are poised to apply dynamic management across numerous marine sectors. Existing examples demonstrate that dynamic management can successfully allow managers to respond rapidly to changes on-thewater, however to implement dynamic ocean management widely, several gaps must be filled. These include enhancing legal instruments, incorporating ecological and socioeconomic considerations simultaneously, developing 'out-of-the-box' platforms to serve dynamic management data to users, and developing applications broadly across additional marine resource sectors.

Johnson, Chris J., **Libby P. W. Ehlers**, Dale R. Seip. 2015. Witnessing extinction – Cumulative impacts across landscapes and the future loss of an evolutionarily significant unit of woodland caribou in Canada. Biological Conservation 186:176-186

Abstract - Habitat change is a major driver of species distribution and persistence, but there have been few recorded extinction events for terrestrial mammals across Canada. Currently, we are observing the decline, extirpation, and perhaps extinction of several evolutionarily significant units of woodland caribou (*Rangifer tarandus caribou*), an iconic and cultural keystone species. We used an extensive set of caribou locations (5 subpopulations, 102 animals, 270,808 GPS-collar locations) collected over 11 years within the Central Mountain Designatable Unit to develop species distribution models that quantified avoidance by caribou of anthropogenic and natural disturbance features. Those empirical relationships allowed us to measure the loss of habitat over a 22-year period and correlate habitat change with measured population decline. The disturbance

responses for caribou were complex and varied by season and subpopulation. We modelled a zone of influence for roads (1.75 km), seismic and pipelines (2.5 km), oil and gas features (4.25 km), cutblocks (5.5 km), burns (8.0 km), and coal mines (3.0 km). When the distribution models for each subpopulation were applied to the respective seasonal ranges, we measured a maximum loss in high-quality habitat of 65.9%. The reduction in habitat was strongly correlated with the annual multiplicative growth rate of 5 subpopulations of caribou. At current rates of habitat loss and population decline, these caribou, a significant component of Canada's biodiversity, are unlikely to persist. Although the factors leading to extinction are complex, the cumulative impacts of industrial development are a correlative if not causative factor.

Week of 20 April 2015

Lyday, S. E., **L. T. Ballance**, D. B. Field, and K. D. Hyrenbach. 2015. Shearwaters as ecosystem indicators: towards fishery-independent metrics of fish abundance in the California Current. Journal of Marine Systems 146:109-120.

Abstract - Shearwaters are ideal for monitoring ocean conditions in the California Current because these predators are abundant, conspicuous, and responsive to oceanographic variability. Herein we evaluated black-vented (Puffinus opisthomelas), Buller's (P. bulleri), flesh-footed (P. carneipes), pinkfooted (P. creatopus), short-tailed (P. tenuirostris), and sooty (P. griseus) shearwaters as fisheryindependent indicators of predatory or prey fish availability. We analyzed four years (1996, 2001, 2005, 2008) of monthly (August–November) National Oceanic and Atmospheric Administration seabird surveys, and United States Geological Survey Pacific Coast Fisheries Database catch, from the California coast to 200 nm offshore. An ordination of shearwater abundance and fish catch revealed that the shearwaters and 11 fish/squid species were significantly correlated with one or more of three principal components, which explained 86% of the variation and revealed distinct species assemblages. We evaluated multiple linear regression models for 19 fisheries using five shearwater metrics: density, aggregation, and behavior (traveling, stationary, feeding), three oceanographic indices, and latitude. Eight of these models had a shearwater metric as the primary predictor. In particular, feeding black-vented shearwater abundance explained 75% of dolphinfish (Coryphaena hippurus) longline catch. This research illustrates the utility of shearwaters as ecosystem indicators, with direct application for predicting fishery catch of commercial importance.

Seminoff, J. A., C. D. Allen, G. H. Balazs, P. H. Dutton, T. Eguchi, H. L. Haas, S.A. Hargrove, M. P. Jensen, D. L. Klemm, A. M. Lauritsen, S. L. MacPherson, P. Opay, E. E. Possardt, S. L. Pultz, E. E. Seney, K. S. Van Houtan, and R. S. Waples. 2015. Status Review of the Green Turtle (*Chelonia mydas*) Under the U.S. Endangered Species Act. NOAA Technical Memorandum, NOAA-NMFS-SWFSC-539. 571pp.

Executive Summary: The green turtle (Chelonia mydas) was listed under the ESA on July 28, 1978. Breeding populations of the green turtle in Florida and along the Pacific Coast of Mexico were listed as endangered; all other populations were listed as threatened. In 2007, the National Marine Fisheries Service (NMFS) and the U.S. Fish and Wildlife Service (USFWS); together the Services completed a 5-year review for the green turtle. A 5-year review is an assessment of a listed species to determine whether its status has changed since the time of its listing such that it should be delisted or classified differently than its current status. The Services concluded that new information available since the completion of the previous reviews indicated a possible separation of populations by ocean basins but that a more in-depth analysis was needed to determine the application of the distinct population segment (DPS) policy. Based on the new information and the need for further analysis under the DPS policy, the Services recommended that no change in listing status was warranted in 2007. However, they committed to fully assemble and analyze all relevant information in accordance with the DPS policy. On February 16, 2012, the Services received a petition from the Association of Hawaiian Civic Clubs to identify the Hawaiian green turtle population as a DPS and delist the DPS under the Endangered Species Act of 1973, as amended (ESA; 16 U.S.C. § 1531 et seq.). On August 1, 2012, NMFS (with USFWS concurrence) determined that the petition presented substantial information indicating that the petitioned action may be warranted and initiated a status review to determine whether the petitioned action is warranted. The Services decided to review the Hawaiian population in the context of examining green turtles globally with regard to application of the DPS policy and in light of significant new information since the listing of the species in 1978. This is consistent with the

recommendation in the 2007 review. The Services convened a status review team (SRT) in November 2012 to review the best available scientific information, determine whether DPSs exist, and assess the extinction risk for any identified DPS. In accordance with the DPS policy, a population may be defined as a DPS if it is both discrete and significant relative to its taxon. With regard to discreteness, the SRT evaluated genetic evidence, tagging (flipper and passive integrated transponder (PIT) tags) and satellite telemetry data, demographics information, oceanographic features, and geographic barriers. It determined that there are 11 discrete population segments for green turtles globally. These discrete population segments are markedly separated from each other as a consequence of ecological, behavioral, and oceanographic factors, and based on genetic and morphological evidence. The SRT then considered whether each of the 11 identified discrete population segments is significant relative to its taxon. The SRT determined that each of the 11 discrete population segments were biologically and ecologically significant. They each represent a large portion of the species range, whose loss would result in a significant gap in distribution of the species. Each discrete population segment is genetically unique; the loss of any one discrete population segment would represent a significant loss of genetic diversity. Further, some DPSs represent unique ecological settings influenced by local ecological and physical factors, some exhibit unique morphological or other demographic characteristics, and others have unique movement patterns. Therefore, the SRT concluded that the 11 identified population segments are both discrete from other conspecific population segments and significant to the species, Chelonia mydas. Although DPS is a legal term and the SRT recognizes that these population segments are not technically DPSs until or unless they are designated as such in a rulemaking process, for lack of a better term, we refer to these units as DPSs throughout the report. The SRT identified the following 11 green turtle DPSs distributed globally: (1) North Atlantic DPS (2) Mediterranean DPS (3) South Atlantic DPS (4) Southwest Indian DPS (5) North Indian DPS (6) East Indian - West Pacific DPS (7) Central West Pacific DPS (8) Southwest Pacific DPS (9) Central South Pacific DPS (10) Central North Pacific DPS (11) East Pacific DPS. After the 11 DPSs were identified, the SRT assessed the extinction risk for each DPS. Six critical assessment elements were considered and quantified in this assessment: (1) abundance; (2) population growth rate or productivity; (3) spatial structure; (4) diversity / resilience; (5) threats (as represented by the five factors in section 4(a)(1) of the ESA); and (6) conservation efforts. Each SRT voting member ranked the importance of each of the population elements (first four above) by assigning them a value from 1 to 5, with 1 representing a very low risk. They ranked the influence of the five factors (threats) on the status of the DPS by assigning a value of 0 (neutral) to -2, and ranked the influence of conservation efforts on the status of the DPS by assigning a value of 0 to 2. The SRT noted that none of these elements is entirely independent, and did not attempt to use the values applied to each element by each SRT member to arrive at extinction risk. In the next step, the SRT reviewed information on threats and extinction risk to portions of the ranges for each DPS that, at present, have substantially higher risk than other parts of the DPS and evaluated if these are significant. A portion of the range of a species is considered to be a significant portion of its range (SPR) if it's contribution to the viability of the species is so important that, if green turtles were extirpated within it, the remaining portion of the population would be in danger of extinction. Only two DPSs were found to have potential SPRs, the Central North Pacific DPS, and the East Indian-West Pacific DPS. Finally, each SRT voting member gave their expert opinion on the likelihood that each DPS would reach a critical risk threshold (quasiextinction) within 100 years by spreading 100 points across several risk categories for each DPS. For DPSs that were determined to have potential SPRs, the SRT conducted two votes for the risk of extinction: One for the entire DPS, and one for the DPS that would remain if the SPR is lost. A summary of the SRT's discussions of the critical assessment elements, overall risk of extinction, and conclusions on SPR for each DPS is found in the DPS-specific sections (Sections 5–15) of this report.

R. S. Waples, P. B. Adams, J. A. Bohnsack, and **B. L. Taylor.** 2015. When is a species at risk in "all or a significant portion of its range"? Endangered Species Research published online. 27: 189-192, doi: 10.3354/esr00669.

Abstract - The US Endangered Species Act (ESA) allows protection of any species that is at risk in all or 'a significant portion of its range' (SPOIR). Because this provision is open to many possible interpretations, the agencies responsible for implementing the ESA recently published a SPOIR policy. The policy is based on a framework we developed that asks a simple question: 'If the portions of the range that are currently at risk were lost, would the entire species, at that point, be threatened or endangered?' If so, the portion of the range is significant. Some commentators have argued that the policy departs from goals the ESA was originally intended to accomplish. We disagree; biologists and managers struggling to implement provisions of the ESA in complex, realworld situations need practical guidance, and we believe our framework provides that. In particular, it avoids as much as possible normative considerations in evaluating 'significance' in terms of human values; instead, we focus on significance to the species, which is consistent with the ESA focus on preventing extinctions, as well as with the mandate that listing determinations be based 'solely' on scientific information. However, we agree with some critics that a crucial factor in implementation of the policy will be how historical versus current concepts of range are reconciled. We believe that historical distribution and abundance are important, not as specific restoration goals, but as reference points that characterize conditions under which we are confident the species was viable.

Week of 23 March 2015

Pardo, Mario A., **T. Gerrodette**, E. Beier, D. Gendron, **K. A. Forney**, **S. J. Chivers**, **J. Barlo**w and D. M. Palacios. 2015. Inferring cetacean population densities from the absolute dynamic topography of the ocean in a hierarchical Bayesian framework. PlosOne DOI:10.1371/journal.pone.0120727.

Abstract - We inferred the population densities of blue whales (Balaenoptera musculus) and shortbeaked common dolphins (Delphinus delphis) in the Northeast Pacific Ocean as functions of the water-column's physical structure by implementing hierarchical models in a Bayesian framework. This approach allowed us to propagate the uncertainty of the field observations into the inference of species-habitat relationships and to generate spatially explicit population density predictions with reduced effects of sampling heterogeneity. Our hypothesis was that the large-scale spatial distributions of these two cetacean species respond primarily to ecological processes resulting from shoaling and outcropping of the pycnocline in regions of wind-forced upwelling and eddy-like circulation. Physically, these processes affect the thermodynamic balance of the water column, decreasing its volume and thus the height of the absolute dynamic topography (ADT). Biologically, they lead to elevated primary productivity and persistent aggregation of low-trophic-level prey. Unlike other remotely sensed variables, ADT provides information about the structure of the entire water column and it is also routinely measured at high spatial-temporal resolution by satellite altimeters with uniform global coverage. Our models provide spatially explicit population density predictions for both species, even in areas where the pycnocline shoals but does not outcrop (e.g. the Costa Rica Dome and the North Equatorial Countercurrent thermocline ridge). Interannual variations in distribution during El Niño anomalies suggest that the population density of both species decreases dramatically in the Equatorial Cold Tongue and the Costa Rica Dome, and that their distributions retract to particular areas that remain productive, such as the more oceanic waters in the central California Current System, the northern Gulf of California, the North Equatorial Countercurrent thermocline ridge, and the more southern portion of the Humboldt Current System. We posit that such reductions in available foraging PLOS habitats during climatic disturbances could incur high energetic costs on these populations, ultimately affecting individual fitness and survival.

Hart CE, Blanco GS, Coyne MS, Delgado-Trejo C, Godley BJ, Jones TT, Resendiz A, **Seminoff JA**, Witt MJ, Nichols WJ. 2015. Multinational Tagging Efforts Illustrate Regional Scale of Distribution and Threats for East Pacific Green Turtles (*Chelonia mydas agassizii*). PLoS ONE 10(2): e0116225.

Abstract - To further describe movement patterns and distribution of East Pacific green turtles (Chelonia mydas agassizii) and to determine threat levels for this species within the Eastern Pacific. In order to do this we combined published data from existing flipper tagging and early satellite tracking studies with data from an additional 12 satellite tracked green turtles (1996-2006). Three of these were tracked from their foraging grounds in the Gulf of California along the east coast of the Baja California peninsula to their breeding grounds in Michoacán (1337-2928 km). In addition, three post-nesting females were satellite tracked from Colola beach, Michoacán to their foraging grounds in southern Mexico and Central America (941.3-3020 km). A further six turtles were tracked in the Gulf of California within their foraging grounds giving insights into the scale of ranging behaviour. Turtles undertaking long-distance migrations showed a tendency to follow the coastline. Turtles tracked within foraging grounds showed that foraging individuals typically ranged up to 691.6 km (maximum) from release site location. Additionally, we carried out threat analysis (using the cumulative global human impact in the Eastern Pacific) clustering pre-existing satellite tracking studies from Galapagos, Costa Rica, and data obtained from this study; this indicated that turtles foraging and nesting in Central American waters are subject to the highest anthropogenic impact. Considering that turtles from all three rookeries were found to migrate towards Central America, it is highly important to implement conservation plans in Central American coastal areas to ensure the survival of the remaining green turtles in the Eastern Pacific. Finally, by combining satellite tracking data from this and previous studies, and data of tag returns we created the best available distributional patterns for this particular sea turtle species, which emphasized that conservation measures in key areas may have positive consequences on a regional scale.

Liles MJ, Peterson MJ, **Seminoff JA**, Altamirano E, Henríquez AV, Gaos AR, Gadea V, Urteaga J, Torres P, Wallace BP, Peterson TR. 2015. One size does not fit all: Importance of adjusting conservation practices for endangered hawksbill turtles to address local nesting habitat needs in the eastern Pacific Ocean. Biological Conservation 184:405–413.

Abstract - Conservation biologists frequently use data from the same or related species collected in diverse geographic locations to guide interventions in situations where its applicability is uncertain. There are dangers inherent to this approach. The nesting habitats of critically endangered hawksbill sea turtles (*Eretmochelys* imbricata) cover a broad geographic global range. Based on data collected in the Caribbean and Indo-Pacific, conservationists assume hawksbills prefer open-coast beaches near coral reefs for nesting, and that individual hawksbills are highly consistent in nest placement, suggesting genetic factors partially account for variation in nest-site choice. We characterized nest-site preferences of hawksbills in El Salvador and Nicaragua, where >80% of nesting activity occurs for this species in the eastern Pacific, and >90% of hawksbill clutches are relocated to hatcheries for protection. We found hawksbills preferred nest sites with abundant vegetation on dynamic beaches within mangrove estuaries. Nests in El Salvador were located closer to the ocean and to the woody vegetation border than nests in Nicaragua, suggesting female hawksbills exhibit local adaptations to differences in nesting habitat. Individual hawksbills consistently placed nests under high percentages of overstory vegetation, but were not consistent in nest placement related to woody vegetation borders. We suggest conservation biologists use caution when generalizing about endangered species that invest in specific life-history strategies (e.g., nesting) over broad ranges based on data collected in distant locations when addressing conservation issues.

Martien, K. K., A. R. Lang, and B. L. Taylor. 2015. Report of the meeting on the use of multiple lines of evidence to delineate demographically independent populations. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-538, 10 p.

Abstract - none. This report covers the Stock Delineation Guidelines Initiative.

Week of 8 March 2015

Summer L. Martin, Stephen M. Stohs, and **Jeffrey E. Moore**. 2015. Bayesian inference and assessment for rare-event bycatch in marine fisheries: a drift gillnet fishery case study. Ecological Applications 25:416–429. http://dx.doi.org/10.1890/14-0059.1

Abstract - Fisheries bycatch is a global threat to marine megafauna. Environmental laws require bycatch assessment for protected species, but this is difficult when bycatch is rare. Low bycatch rates, combined with low observer coverage, may lead to biased, imprecise estimates when using standard ratio estimators. Bayesian model-based approaches incorporate uncertainty, produce less volatile estimates, and enable probabilistic evaluation of estimates relative to management thresholds. Here, we demonstrate a pragmatic decision-making process that uses Bayesian model-based inferences to estimate the probability of exceeding management thresholds for bycatch in fisheries with <100% observer coverage. Using the California drift gillnet fishery as a case study, we (1) model rates of rare-event bycatch and mortality using Bayesian Markov chain Monte Carlo estimation methods and 20 years of observer data; (2) predict unobserved counts of bycatch and mortality; (3) infer expected annual mortality; (4) determine probabilities of mortality exceeding regulatory thresholds; and (5) classify the fishery as having low, medium, or high bycatch impact using those probabilities. We focused on leatherback sea turtles (Dermochelys coriacea) and humpback whales (Megaptera novaeangliae). Candidate models included Poisson or zero-inflated Poisson likelihood, fishing effort, and a bycatch rate that varied with area, time, or regulatory regime. Regulatory regime had the strongest effect on leatherback bycatch, with the highest levels occurring prior to a regulatory change. Area had the strongest effect on humpback bycatch. Cumulative bycatch estimates for the 20-year period were 104–242 leatherbacks (52–153 deaths) and 6–50 humpbacks (0-21 deaths). The probability of exceeding a regulatory threshold under the U.S. Marine Mammal Protection Act (Potential Biological Removal, PBR) of 0.113 humpback deaths was 0.58, warranting a "medium bycatch impact" classification of the fishery. No PBR thresholds exist for leatherbacks, but the probability of exceeding an anticipated level of two deaths per year, stated as part of a U.S. Endangered Species Act assessment process, was 0.0007. The approach demonstrated here would allow managers to objectively and probabilistically classify fisheries with respect to bycatch impacts on species that have population-relevant mortality reference points, and declare with a stipulated level of certainty that bycatch did or did not exceed estimated upper bounds.

Klueter, A.; Crandall, J.B.; **Archer, F.I.**; Teece, M.A.; Coffroth, M.A. 2015. Taxonomic and Environmental Variation of Metabolite Profiles in Marine Dinoflagellates of the Genus Symbiodinium. Metabolites 5, 74-99. http://www.mdpi.com/2218-1989/5/1/74/

Abstract - Microorganisms in terrestrial and marine ecosystems are essential to environmental sustainability. In the marine environment, invertebrates often depend on metabolic cooperation with their endosymbionts. Coral reefs, one of the most important marine ecosystems, are based on the symbiosis between a broad diversity of dinoflagellates of the genus Symbiodinium and a wide phyletic diversity of hosts (i.e., cnidarian, molluscan, poriferan). This diversity is reflected in the ecology and physiology of the symbionts, yet the underlying biochemical mechanisms are still poorly understood. We examined metabolite profiles of four cultured species of Symbiodinium known to form viable symbioses with reef-building corals, S. microadriaticum (cp-type A194), S. minutum (cp-type B184), S. psygmophilum (cp-type B224) and S. trenchii (cp-type D206). Metabolite profiles were shown to differ among Symbiodinium species and were found to be affected by their physiological response to growth in different temperatures and light regimes. A combined Random Forests and Bayesian analysis revealed that the fourSymbiodinium species examined primarily differed in their production of sterols and sugars, including a C29 stanol and the two sterols C28 Δ 5 and C28 Δ 5,22, as well as differences in metabolite abundances of a hexose and inositol. Inositol levels were also strongly affected by changes in temperature across all Symbiodinium species. Our results offer a detailed view of the metabolite profile characteristic of marine symbiotic dinoflagellates of the genus Symbiodinium, and identify patterns of metabolites related to several growth conditions.

Forney, K.A., E.A. Becker, D. Foley, **J. Barlow**, and E.M. Oleson. 2015. Habitat-based models of cetacean density and distribution in the central North Pacific. Endangered Species Research Vol. 27: 1–20. Contribution to the Theme Section 'Geospatial approaches to support pelagic conservation planning and adaptive management. [doi: 10.3354/esr00632]

Abstract - The central North Pacific Ocean includes diverse temperate and tropical pelagic habitats. Studies of the abundance and distribution of cetaceans within these dynamic marine ecosystems have generally been patchy or conducted at coarse spatial and temporal scales, limiting their utility for pelagic conservation planning. Habitat-based density models provide a tool for identifying pelagic areas of importance to cetaceans, because model predictions are spatially explicit. In this study, we present habitat-based models of cetacean density that were developed and validated for the central North Pacific. Spatial predictions of cetacean densities and measures of uncertainty were derived based on data collected during 15 large-scale shipboard cetacean and ecosystem assessment surveys conducted from 1997 to 2012. We developed generalized additive models using static and remotely sensed dynamic habitat variables, including distance to land, sea-surface temperature (SST), standard deviation of SST, surface chlorophyll concentration, sea-surface height (SSH), and SSH root-mean-square variation. The resulting models, developed using new grid-based prediction methods, provide finer scale information on the distribution and density of cetaceans than previously available. Habitat-based abundance estimates around Hawaii are similar to those derived from standard line-transect analyses of the same data and provide enhanced spatial resolution to inform management and conservation of pelagic cetacean species.

Week of 16 February 2015

Goebel, M. E., **Perryman, W. L.**, Hinke, J. T., Krause, D. J., Hann, N. A., Gardner, S., & LeRoi, D. J. A small unmanned aerial system for estimating abundance and size of Antarctic predators. Polar Biology 1-12.

Abstract - Quantifying the distribution and abundance of predators is integral to many ecological studies, but can be difficult in remote settings such as Antarctica. Recent advances in the development of unmanned aerial systems (UAS), particularly vertical takeoff and landing (VTOL) aircraft, have provided a new tool for studying the distribution and abundance of predator populations. We detail our experience and testing in selecting a VTOL platform for use in remote, windy, perennially overcast settings, where acquiring cloud-free high-resolution satellite images is often impractical. We present results from the first use of VTOLs for estimating abundance, colony area, and density of krill-dependent predators in Antarctica, based upon 65 missions flown in 2010/2011 (n = 28) and 2012/2013 (n = 37). We address concerns over UAS sound affecting wildlife by comparing VTOL-generated noise to ambient and penguin-generated sound. We also report on the utility of

VTOLs for missions other than abundance and distribution, namely to estimate size of individual leopard seals. Several characteristics of small, battery-powered VTOLs make them particularly useful in wildlife applications: (1) portability, (2) stability in flight, (3) limited launch area requirements, (4) safety, and (5) limited sound when compared to fixed-wing and internal combustion engine aircraft. We conclude that of the numerous UAS available, electric VTOLs are among the most promising for ecological applications.

Kellar, N. M., Catelani, K. N., Robbins, M. N., Trego, M. L., Allen, C. D., Danil, K., and Chivers, S. J. (2015). Blubber Cortisol: A Potential Tool for Assessing Stress Response in Free-Ranging Dolphins without Effects due to Sampling. PloS one, 10(2), e0115257.

Abstract - When paired with dart biopsying, quantifying cortisol in blubber tissue may provide an index of relative stress levels (i.e., activation of the hypothalamus-pituitary-adrenal axis) in free-ranging cetacean populations while minimizing the effects of the act of sampling. To validate this approach, cortisol was extracted from blubber samples collected from beach-stranded and by caught short-beaked common dolphins using a modified blubber steroid isolation technique and measured via commercially available enzyme immunoassays. The measurements exhibited appropriate quality characteristics when analyzed via a bootstraped stepwise parallelism analysis (observed/expected = 1.03, 95% CI: 99.6 - 1.08) and showed no evidence of matrix interference with increasing sample size across typical biopsy tissue masses (75–150mg; r₂ = 0.012, p = 0.78, slope = 0.022ngcortisol deviation/ultissue extract added). The relationships between blubber cortisol and eight potential cofactors namely, 1) fatality type (e.g., stranded or bycaught), 2) specimen condition (state of decomposition), 3) total body length, 4) sex, 5) sexual maturity state, 6) pregnancy status, 7) lactation state, and 8) adrenal mass, were assessed using a Bayesian generalized linear model averaging technique. Fatality type was the only factor correlated with blubber cortisol, and the magnitude of the effect size was substantial: beach-stranded individuals had on average 6.1-fold higher cortisol levels than those of bycaught individuals. Because of the difference in conditions surrounding these two fatality types, we interpret this relationship as evidence that blubber cortisol is indicative of stress response. We found no evidence of seasonal variation or a relationship between cortisol and the remaining cofactors.

Week of 9 February 2015

Priddel, D., N. Carlile, D. Portelli, Y. Kim, L. O'Neill, V. Bretagnolle, **L.T. Ballance**, R.A. Phillips, R.L. Pitman, M.J. Rayner. 2014. Pelagic distribution of Gould's Petrel *Pterodroma leucoptera*: linking shipboard and beached bird sightings with remote tracking data. Emu 114: 360-370.

Abstract - This study describes and compares the pelagic distribution and migratory patterns of the two subspecies of Gould's Petrel (*Pterodroma leucoptera*), and contrasts data obtained from tracking birds at sea using geolocators with observational data (shipboard sightings, by-catch records and beachcast specimens). While breeding, tracked individuals of both subspecies (*P. l. leucoptera* and *P. l. caledonica*) foraged within the Tasman Sea and south of the Australian continent, with forays west into the Indian Ocean before laying. After breeding, both subspecies migrated to distinct non-breeding ranges within the eastern tropical Pacific Ocean. Observational data identified the general pattern of migration and foraging areas of the species, whereas data from geolocators provided details of routes and timing of migration, core foraging ranges, and marked spatial and temporal segregation between the two subspecies. However, by attaching geolocators only to established breeders, as is typical of studies of small and medium-sized seabirds, these devices failed to identify that nonbreeding birds (pre-breeders and adults that are deferring breeding) may not follow the same migratory schedules or have the same at-sea distribution. We conclude that integrating data from electronic tracking with observational data substantially improves our understanding of the pelagic distribution of seabird populations.

Martien, K.K., D.P. Gregovich, and A.E. Punt. 2013. Defining the appropriate 'Unit-To-Conserve' under the International Whaling Commission's Revised Management Procedure. Journal of Cetacean Research and Management 13(1): 31-38.

Abstract - Identifying the appropriate 'Unit to Conserve' (UTC) is critical to the success of any management scheme. While the need to define the UTC appropriate to the IWC's Catch Limit Algorithm (CLA) has long

been recognized by its Scientific Committee, little progress has been made on this issue. The CLA was rigorously tested prior to its adoption. However, most of those original performance trials focused on singlepopulation scenarios or two-population scenarios with no ongoing dispersal. None of the trials considered the performance of the CLA across a range of dispersal rates. In this study, the performance of the CLA under a variety of population structure scenarios is examined. This is the first study to investigate the levels of connectivity (i.e. dispersal rate) for which populations require separate management to meet the conservation goals of the CLA. All the trials consisted of two populations that were managed as a single stock for 100 years. Both historical and modern hunts were spatially-biased so that population 1 was the primary target of hunting. Parameters that varied among trials were the relative carrying capacities (K) of the populations, the dispersal rate between them, maximum sustainable yield rate (MSYR1+), and the precision in simulated abundance estimates. All of these parameters had strong effects on the conservation performance of the CLA. Trials with a low MSYR1+ (1%) generally ended with the abundance of population 1 below 0.54K, regardless of the dispersal rate or relative carrying capacities of the two populations. The same was true of trials in which the carrying capacity of population 1 represented only 10% of the total landscape carrying capacity and the CV of the abundance estimates was low, even when dispersal between populations was high $(5 \times 10-3\text{yr}-1)$ and MSYR1+ was 4%. The results suggest that the appropriate UTCs under the RMP are likely to exchange dispersers at high enough rates that they will be difficult to delineate using existing methods. These results also highlight the value of spatially-diffuse hunting patterns that avoid potential overhunting of unrecognised stocks.

Week of 2 February 2015

Draft Marine Mammal Stock Assessment Reports (SARs) - the 2014 draft Marine Mammal Stock Assessment Report Reports were published on January 29, 2015 (80 FR 4881) and close for comment on April 29, 2015. The multi-authored U.S. Pacific SAR (James V. Carretta, Erin Oleson, Dave W. Weller, Aimee R. Lang, Karin A. Forney, Jason Baker, Brad Hanson, Karen Martien, Marcia M. Muto, Anthony J. Orr, Harriet Huber, Mark S. Lowry, Jay Barlow, Jeffrey E. Moore, Deanna Lynch, Lilian Carswell, Robert L. Brownell Jr., and David K. Mattila) can be accessed online at http://www.nmfs.noaa.gov/pr/sars/draft.htm.

Week of 19 January 2015

Andrew D. Foote and **Phillip A. Morin**. 2015. Letter to the Editor in response to Moura et al. Sympatric speciation in killer whales? Heredity doi:10.1038/hdy.2014.120.

In a recent study published in Heredity, Moura et al. (2014) claim their phylogenomic analysis of historical biogeography indicates that killer whale ecotypes found in the largest ocean basin, the North Pacific, diverged in sympatry. We contend that Moura et al.'s inference of divergence within the Pacific Ocean do not equate to divergence in sympatry, and discuss alternative interpretations of their results. Both the mitochondrial and nuclear phylogenies from Moura et al. are compatible with several biogeographical histories of varying complexity, and the most likely history under one evolutionary model may not necessarily be the true history. The data, however, will allow further investigation of some of this uncertainty and the comparison of different models including those that consider gene flow upon secondary contact, providing further insight into the diversification process of killer whales.

Shaul, Nellie J., Nathan G. Dodder, Lihini I. Aluwihare, Susan Mackintosh, Keith Maruya, **Susan J. Chivers, Kerri Danil**, **Dave W. Weller**, and Eunha Hoh. 2015. Nontargeted biomonitoring of halogenated organic compounds in two ecotypes of bottlenose dolphins (*Tursiops truncatus*) from the Southern California Bight. Environmental Science and Technology. DOI: 10.1021/es50516q. Available on line at: http://pubs.acs.org/articlesonrequest/AOR-eNRU6kiDBXE55cYAI5nd.

Abstract: Targeted environmental monitoring reveals contamination by known chemicals, but may exclude potentially pervasive but unknown compounds. Marine mammals are sentinels of persistent and bioaccumulative contaminants due to their longevity and high trophic position. Using nontargeted analysis, we constructed a mass spectral library of 327 persistent and bioaccumulative compounds identified in blubber from two ecotypes of common bottlenose dolphins (*Tursiops truncatus*) sampled in the Southern California Bight.

This library of halogenated organic compounds (HOCs) consisted of 180 anthropogenic contaminants, 41 natural products, 4 with mixed sources, 8 with unknown sources, and 94 with partial structural characterization and unknown sources. The abundance of compounds whose structures could not be fully elucidated highlights the prevalence of undiscovered HOCs accumulating in marine food webs. Eighty-six percent of the identified compounds are not currently monitored, including 133 known anthropogenic chemicals. Compounds related to dichlorodiphenyltrichloroethane

(DDT) were the most abundant. Natural products were, in some cases, detected at abundances similar to anthropogenic compounds. The profile of naturally occurring HOCs differed between ecotypes, suggesting more abundant offshore sources of these compounds. This nontargeted analytical framework provided a comprehensive list of HOCs that may be characteristic of the region, and its application within monitoring surveys may suggest new chemicals for evaluation.

Week of 22 December 2014

Vu, E.T., C. Clark, **K. Catelani**, **N. M. Kellar**, and J. Calambokidis. 2014. Seasonal blubber testosterone concentrations of male humpback whales (*Megaptera novaeangliae*). Marine Mammal Science. DOI: 10.1111/mms.12191 [no abstract].

Week of 15 December 2014

Joseph R. Jehl, Jr, **Annette E. Henry** and David L. Swanson. 2014. Ratios, adaptations, and the differential metabolic capability of avian flight muscles. J. Avian Biology 45: 1-6.

Abstract - The eared grebe *Podiceps nigricollis* shows seasonal variation in the relative size of the major flight muscles that lift and lower the wing: respectively, supracoracoideus (s) and pectoralis (p). S/p ratios are low (≈ 0.07 –0.12) when grebes are in flying condition, higher (≈ 0.11 –0.15) when staging and flightless, and extreme (to 0.29) when starving. Shifts were driven by changes in the protein content in the pectoralis; intramuscular fat had little effect. S/p ratios also vary seasonally in the red knot *Calidris canutus* and are higher in birds newly arrived in breeding areas than at other times. If that increase was an adaptive response to promote wing-lifting in association with various breeding behaviors as suggested, one would expect it to result from an absolute increase in the post-arrival size of the supracoracoideus, which was not observed. Instead, we propose that it is unrelated to enhancing the upstroke but results from a decrease in the size of the pectoralis, which is a consequence of the greater rate at which this muscle is catabolized in times of exertion and stress, as at the end of a long migration or during starvation. Fuller data on the size, morphology and physiology of individual muscles at various stages

of the annual cycle and migration will help to clarify how ratio changes are achieved, and evaluate potential adaptive significance. http://onlinelibrary.wiley.com/doi/10.1111/jav.00506/abstract.

C. Pomilla, A. R. Amaral, T. Collins, G. Minton, K. Findlay, **Matthew S. Leslie,** L. Ponnampalam, R. Baldwin, H. Rosenbaum. 2014. The world's most isolated and distinct whale population? Humpback whales of the Arabian Sea. PLOS ONE. http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0114162

Abstract - A clear understanding of population structure is essential for assessing conservation status and implementing management strategies. A small, non-migratory population of humpback whales in the Arabian Sea is classified as "Endangered" on the IUCN Red List of Threatened Species, an assessment constrained by a lack of data, including limited understanding of its relationship to other populations. We analyzed 11 microsatellite markers and mitochondrial DNA sequences extracted from 67 Arabian Sea humpback whale tissue samples and compared them to equivalent datasets from the Southern Hemisphere and North Pacific. Results show that the Arabian Sea population is highly distinct; estimates of gene flow and divergence times suggest a Southern Indian Ocean origin but indicate that it has been isolated for approximately 70,000 years, remarkable for a species that is typically highly migratory. Genetic diversity values are significantly lower than those obtained for Southern Hemisphere populations and signatures of ancient and recent genetic bottlenecks were identified. Our findings suggest this is the world's most isolated humpback whale population, which, when combined with low population abundance estimates and anthropogenic threats, raises concern for its survival. We recommend an amendment of the status of the population to Critically Endangered on the IUCN Red List.

Week of 8 December 2014

Calderan, S., B. Miller, K. Collins, P. Ensor, M. Double, R. Leaper, and J. **Barlow**. 2014. Low frequency vocalizations of sei whales (*Balaenoptera borealis*) in the Southern Ocean. Journal Acoustical Society of America 136(6):EL418. *Abstract*: Simultaneous sightings and acoustic detections of sei whales (*Balaenoptera borealis*) are scarce, and there are few published data describing their vocalizations. Analysis of recordings from directional frequency analysis and recording sonobuoys in the presence of sei whales in the Southern Ocean in March 2013 identified both downsweep and upsweep calls. Sound frequencies within all calls were between 34 and 87 Hz with an average call duration of 1.1 s. These very low-frequency sounds share characteristics with sei whale calls recorded near the Hawaiian Islands and off Cape Cod in winter and summer, respectively, but are the first documented sei whale calls in the Southern Ocean that are clearly less than 100 Hz.

Week of 1 December 2014

Pitman, R.L., J.A. Totterdell, **H. Fearnbach**, **L.T. Ballance**, **J.W. Durban**, and H. Kemps. 2014. Whale killers: Prevalence and ecological implications of killer whale predation on humpback whale calves off Western Australia. Marine Mammal Science DOI: 10.1111/mms.12182

Abstract - Reports of killer whales (*Orcinus orca*) preying on large whales have been relatively rare, and the ecological significance of these attacks is controversial. Here we report on numerous observations of killer whales preying on neonate humpback whales (Megaptera novaeangliae) off Western Australia (WA) based on reports we compiled and our own observations. Attacking killer whales included at least 19 individuals from three stable social groupings in a highly connected local population; 22 separate attacks with known outcomes resulted in at least 14 (64%) kills of humpback calves. We satellite-tagged an adult female killer whale and followed

her group on the water for 20.3 h over six separate days. During that time, they attacked eight humpback calves, and from the seven known outcomes, at least three calves (43%) were killed. Overall, our observations suggest that humpback calves are a predictable, plentiful, and readily taken prey source for killer whales and scavenging sharks off WA for at least 5 mo/yr. Humpback "escorts" vigorously assisted mothers in protecting their calves from attacking killer whales (and a white shark, Carcharodon carcharias). This expands the purported role of escorts in humpback whale social interactions, although it is not clear how this behavior is adaptive for the escorts.

Week of 3 November 2014

Dutton PH, Jensen MP, Frey A, LaCasella E, Balazs GH, Zárate P, Chassin-Noria O, Sarti-Martinez AL, Velez E. 2014. Population structure and phylogeography reveal pathways of colonization by a migratory marine reptile (*Chelonia mydas*) in the central and eastern Pacific. Ecology and Evolution. doi: 10.1002/ece3.1269.

Abstract - Climate, behavior, ecology and oceanography shape patterns of biodiversity in marine faunas in the absence of obvious geographic barriers. Marine turtles are an example of highly migratory creatures with deep evolutionary lineages and complex life histories that span both terrestrial and marine environments. Previous studies have focused on the deep isolation of evolutionary lineages (>3mya) through vicariance; however little attention has been given to the pathways of colonization of the eastern Pacific and the processes that have shaped diversity within the most recent evolutionary time. We sequenced 770 bp of the mtDNA control region to examine the stock structure and phylogeography of 550 green turtles from eight different rookeries in the central and eastern Pacific. We found significant differentiation between the geographically separated nesting populations and identified five distinct stocks ($F_{ST} = 0.08 - 0.44$, p<0.005). Central and eastern Pacific *Chelonia* mydas form a monophyletic group containing 3 sub-clades, with Hawaii more closely related to the eastern Pacific than western Pacific populations. The split between sampled central/eastern and western Pacific haplotypes was estimated at 0.336 mya, suggesting that the Pacific region west of Hawaii has been a more formidable barrier to gene flow in *C.mydas* than the East Pacific Barrier. Our results suggest that the eastern Pacific was colonized from the western Pacific via the Central North Pacific and that the Revillagigedos Islands provided a stepping-stone for radiation of green turtles from the Hawaiian Archipelago to the eastern Pacific. Our results fit with a broader paradigm that has been described for marine biodiversity, where oceanic islands,

such as Hawaii and Revillagigedos, rather than being peripheral "graveyards", serve as sources and recipients of diversity and provide a mechanism for further radiation.

Week of 27 October 2014

Baird, R. W., S. D. Mahaffy, A. M. Gorgone, T. Cullins, D. J. McSweeney, E. M. Oleson, A. L. Bradford, J. **Barlow**, D. L. Webster. 2014. False killer whales and fisheries interactions in Hawaiian waters: Evidence for sex bias and variation among populations and social groups. Marine Mammal Science.

Abstract - We assessed scarring patterns as evidence of fisheries interactions for three populations of false killer whales in Hawai'i. Bycatch of the pelagic population in the tuna longline fishery exceeds their Potential Biological Removal level. Scarring was assessed by seven evaluators as consistent, possibly consistent, or not consistent with fisheries interactions, and average scores computed. Scores were highest for scarred main Hawaiian Island (MHI) false killer whales, followed by pelagic and Northwestern Hawaiian Island (NWHI) individuals. Considering only whales for which the majority of evaluators scored scarring as consistent revealed significant differences among populations in the percentage of individuals scarred; MHI: 7.5%, pelagic:

0%, NWHI: 0%. Assessment by social cluster for the MHI population showed that 4.2% of Cluster 1, 7.1% of Cluster 2, and 12.8% of Cluster 3 individuals had such scarring, although differences between clusters were not statistically significant. There was a significant sex bias; all sexed individuals (n = 7) with injuries consistent with fisheries interactions were female. The higher proportion of MHI individuals with fisheries-related scarring suggests that fisheries interactions are occurring at a higher rate in this population. The bias towards females suggests that fisheries-related mortality has a disproportionate impact on population dynamics.

Ivashchenko, Y.V., **Brownell, R.L**. Jr. & Clapham, P.J. 2014. Distribution of Soviet catches of sperm whales (*Physeter macrocephalus*) in the North Pacific. Endangered Species Research 25: 249-263.

Abstract - From 1948 to 1979, the USSR conducted extensive illegal whaling worldwide. Data from the North Pacific (NP) were analyzed to correct falsified International Whaling Commission catch records, and to investigate the distribution of sperm whales (NP catch = 157,680). Information was available on the distribution of 123,264 sperm whale catches. Among a number of areas defined by the Soviet whalers the largest catches were in the three main regions: 31,395 in the Eastern Region (ER), 29,518 in the Central Region (CR), 19,313 in the Western Region (WR); an additional 23,090 catches were made at the Kuril land stations. Other areas with substantial catches included the Aleutians (5,945) and Commander Islands (1,448), Bering Sea (3,170), Olyutorsky Bay (3,094), and other parts of the pelagic NP (6,049). Four main areas of concentration included: a large pelagic area (30-50°N) in the ER, including the Gulf of Alaska and western coast of North America; the northeastern and southwestern CR; and the southern Kurils. Some of the distribution was similar to 19th century catches, notably in the "Japan Ground" (in the pelagic western Pacific) and the "Coast of Japan Ground". Many females were caught in Olyutorsky Bay and around the Commander Islands. There was also a division in catch composition at Amchitka Pass (Aleutians), with family groups to the west and mature males to the east. The extensive illegal catches of females removed a significant portion of the reproductively mature population, which likely continues to impact recovery of NP sperm whales today.

This paper is Open Access and a pdf can be downloaded for free at: http://www.int-res.com/abstracts/esr/v25/n3/

Kellar NM, Trego ML, Chivers SJ, Archer FI, Perryman WL (2014) From progesterone in biopsies to estimates of pregnancy rates: Large scale reproductive patterns of two sympatric species of common dolphin, *Delphinus* spp. off California, USA and Baja, Mexico. Bulletin, Southern California Academy of Sciences 113: 58-80

Abstract - Blubber progesterone levels were measured in biopsy samples and used to predict the pregnancy status of 507 female common dolphins (204 long-beaked common dolphins, *Delphinus capensis*, and 303 short-beaked common dolphins, *D. delphis*). Samples were collected in the coastal waters of the eastern North Pacific between central California, USA and the southern end of Baja California, Mexico. The percentage of females pregnant was similar between the two species: 22.1% (n = 45) of *D. capensis* and 28.1% (n = 85) of *D. delphis*. For both species we found strong geographic patterns in pregnancy, suggesting that some areas were more conducive for pregnant females. A sizable drop in percent pregnant from early (38.8%, n = 133) to late (25.3%, n = 91) autumn was found in *D. delphis* but not in *D. capensis*. The potential for sample selectivity was examined via biopsies collected either from a large research ship or from a small, rigid-hull inflatable boat

(RHIB) launched from the larger ship. An analysis of "Tandem Biopsy Sampling", replicate biopsy effort on the same schools from each vessel/platform, yielded little evidence that disproportionately more pregnant female common dolphins were biopsied from one platform versus the other. This result plus an analysis of pregnancy status relative to the duration of biopsy operations failed to uncover strong evidence of unaccounted sampling bias with respect to pregnancy state. In total, these results demonstrate the utility of blubber progesterone concentrations to assess pregnancy status in free-ranging cetaceans and they highlight potential factors associated with population-level variation in dolphin pregnancy rates.

Rocio I. Ruiz-Cooley, Paul L. Koch, **Paul C. Fiedler**, Matthew D. McCarthy. 2014. Carbon and Nitrogen Isotopes from Top Predator Amino Acids Reveal Rapidly Shifting Ocean Biochemistry in the Outer California Current. PLoS ONE 9(10): e110355. doi:10.1371/journal.pone.0110355

Abstract - Climatic variation alters biochemical and ecological processes, but it is difficult both to quantify the magnitude of such changes, and to differentiate long-term shifts from inter-annual variability. Here, we simultaneously quantify decade-scale isotopic variability at the lowest and highest trophic positions in the offshore California Current System (CCS) by measuring d15N and d13C values of amino acids in a top predator, the sperm whale (Physeter macrocephalus). Using a time series of skin tissue samples as a biological archive, isotopic records from individual amino acids (AAs) can reveal the proximate factors driving a temporal decline we observed in bulk isotope values (a decline of \$1 %) by decoupling changes in primary producer isotope values from those linked to the trophic position of this toothed whale. A continuous decline in baseline (i.e., primary producer) d15N and d13C values was observed from 1993 to 2005 (a decrease of ,4% for d15N source-AAs and 3% for d13C essential-AAs), while the trophic position of whales was variable over time and it did not exhibit directional trends. The baseline d15N and d13C shifts suggest rapid ongoing changes in the carbon and nitrogen biogeochemical cycling in the offshore CCS, potentially occurring at faster rates than longterm shifts observed elsewhere in the Pacific. While the mechanisms forcing these biogeochemical shifts remain to be determined, our data suggest possible links to natural climate variability, and also corresponding shifts in surface nutrient availability. Our study demonstrates that isotopic analysis of individual amino acids from a top marine mammal predator can be a powerful new approach to reconstructing temporal variation in both biochemical cycling and trophic structure.

Week of 20 October 2014

Danil, K., J.A. St. Leger, S. Dennison, Y. Bernaldo de Quirós, M. Scadeng, E. Nilson, and N. Beaulieu. 2014. Clostridium perfringens septicemia in a long-beaked common dolphin Delphinus capensis: an etiology of gas bubble accumulation in cetaceans. Diseases of Aquatic Organisms 111:183-190. http://www.int-res.com/abstracts/dao/v111/n3/ Abstract – An adult female long-beaked common dolphin Delphinus capensis live-stranded inLa Jolla, California, USA, on July 30, 2012 and subsequently died on the beach. Computed tomography and magnetic resonance imaging revealed gas bubble accumulation in the vasculature, organ parenchyma, mandibular fat pads, and subdermal sheath as well as a gas-filled cavity within the liver, mild caudal abdominal effusion, and fluid in the uterus. Gross examination confirmed these findings and also identified mild ulcerations on the palate, ventral skin, and flukes, uterine necrosis, and multifocal parenchymal cavitations in the brain. Histological review demonstrated necrosis and round clear spaces interpreted as gas bubbles with associated bacterial rods within the brain, liver, spleen, and lymph nodes. Anaerobic cultures of the lung, spleen, liver, bone marrow, and abdominal fluid yielded Clostridium perfringens, which was further identified as type A via a multiplex PCR assay. The gas composition of sampled bubbles was typical of putrefactiongases, which is consistent with the by-products of C. perfringens, a gas-producing bacterium. Gas bubble formation in marine mammals due to barotrauma, and peri- or postmortem offgassing of supersaturated tissues and blood has been previously described. This case study concluded that a systemic infection of C. perfringens likely resulted in production of gas and toxins, causing tissue necrosis.

Schakner, Z.A., C. Lunsford, J. Straley, **T. Eguchi**, and **S. Mesnick.** 2014. Using models of social transmission to examine the spread of longline depredation behavior among sperm whales in the Gulf of Alaska. PLoS ONE 9(10): e109079.

doi:10.1371/journal.pone.0109079

Abstract – Fishing, farming and ranching provide opportunities for predators to prey on resources concentrated by humans, a behavior termed depredation. In the Gulf of Alaska, observations of sperm whales depredating on

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fish caught on demersal longline gear dates back to the 1970s, with reported incidents increasing in the mid-1990s. Sperm whale depredation provides an opportunity to study the spread of a novel foraging behavior within a population. Data were collected during National Marine Fisheries Service longline surveys using demersal longline gear in waters off Alaska from 1998 to 2010. We evaluated whether observations of depredation fit predictions of social transmission by fitting the temporal and spatial spread of new observations of depredation to the Wave of Advance model. We found a significant, positive relationship between time and the distance of new observations from the diffusion center ($r^2 = 0.55$, p-value = 0.003). The data provide circumstantial evidence for social transmission of depredation. We discuss how changes in human activities in the region (fishing methods and regulations) have created a situation in which there is spatial-temporal overlap with foraging sperm whales, likely influencing when and how the behavior spread among the population.

Week of 6 October 2014

Cheney, Corkrey, **Durban**, Grellier, Hammond, Islas-Villanueva, Janik, Lusseau, Parsons, Quick, Wilson and Thompson. 2014. Long-term trends in the use of a protected area by small cetaceans in relation to changes in population status. Global Ecology and Conservation 2: 118-128. http://dx.doi.org/10.1016/j.gecco.2014.08.010

Abstract -- The requirement to monitor listed species in European designated sites is challenging for long-lived mobile species that only temporarily occupy protected areas. We use a 21 year time series of bottlenose dolphin photo-identification data to assess trends in abundance and conservation status within a Special Area of Conservation (SAC) in Scotland. Mark—recapture methods were used to estimate annual abundance within the SAC from 1990 to 2010. A Bayesian mark—recapture model with a state-space approach was used to estimate overall population trends using data collected across the populations' range. Despite interannual variability in the number of dolphins within the SAC, there was a >99% probability that the wider population was stable or increasing. Results indicate that use of the SAC by the wider population has declined. This is the first evidence of long-term trends in the use of an EU protected area by small cetaceans in relation to changes in overall population status. Our results highlight the importance of adapting the survey protocols used in long-term photo-identification studies to maintain high capture probabilities and minimise sampling heterogeneity. Crucially, these data demonstrate the value of collecting data from the wider population to assess the success of protected areas designated for mobile predators.

Week of 29 September 2014

Martien, K. K., M. C. Hill, A. M. Van Cise, K. M. Robertson, S. M. Woodman, L. Dolar, V. L. Pease, and E. M. Oleson. 2014. Genetic diversity and population structure in four species of cetaceans around the Mariana Islands. U.S. Department of Commerce, NOAA Technical Memorandum NMFS-SWFSC-536. 18 p.

Abstract – Relatively little is known about cetaceans inhabiting the waters of the Mariana Islands in the western Pacific. We use mitochondrial DNA (mtDNA) sequences obtained from biopsy samples to investigate the genetic diversity and structure of four species of delphinids found near the Mariana Islands - short-finned pilot whales (SFPWs; Globicephala macrorhynchus; n=47), spinner dolphins (Stenella longirostris longirostris; n=95), bottlenose dolphins (Tursiops truncatus; n=15), and melon-headed whales (MHWs; Peponocephala electra; n=2). We found evidence of genetic differentiation between islands for SFPWs, but not for spinner dolphins. Sample sizes were too small to investigate differentiation within the other two species. SFPWs around the Marianas possess haplotypes also common in the South Pacific, North Atlantic, Indian Ocean, and off of southern Japan. Both spinner dolphins and MHWs possess haplotypes common throughout the Pacific. The spinner dolphins exhibit high haplotypic diversity similar to that observed in the Society Islands of French Polynesia, suggesting they are not as genetically isolated as Hawaiian spinner dolphins. We did not find any T. aduncus haplotypes among the bottlenose dolphin samples, instead finding that two-thirds of the animals possess T. truncatus haplotypes while the remaining one-third share a single Fraser's dolphin (Lagenodlephis hosei) haplotype. Photo-identification data confirm that the five samples with Fraser's dolphin haplotypes come from five different individuals, all of which appear morphologically to be bottlenose dolphins. This result suggests that there has been extensive introgression of Fraser's dolphin mtDNA into the Mariana Islands bottlenose dolphin gene pool.

Moore, **J.E.**, and **J.P. Barlow**. 2014. Improved abundance and trend estimates for sperm whales in the eastern North Pacific from Bayesian hierarchical modeling. Endangered Species Research 25: 141-150.

ABSTRACT: Population abundance and trends are informative metrics for assessing population status and basing management decisions, but it can be challenging to estimate these metrics for species that are difficult to detect. We used a Bayesian hierarchical approach to improve estimates of abundance and trends for sperm whales *Physeter macrocephalus* in the California Current based on 6 surveys conducted from 1991 to 2008. The method consists either of a regression trend or Markov process model for true abundance in the study area and an observation model used to estimate detection probability (in our case, based on line-transect distance sampling methods). Our approach improves upon models that we have applied to other cetacean species by incorporating direct estimates of sampling variance in the number of groups encountered (to reduce estimates of process variance) and by using an alternative to the commonly used Horvitz-Thompson-like estimator to better deal with covariate-dependent detection probability estimation when sample sizes are small. Our abundance estimates were much less variable through time than previously published estimates; this has important implications for management under the US Marine Mammal Protection Act. We were unable to precisely estimate overall abundance trends for sperm whales in the study area, but we estimated a high probability that small-group abundance, likely representing adult male abundance, has increased.

Week of 22 September 2014

Carretta, J.V., S.M. Wilkin, M.M. Muto, K. Wilkinson, and **J. Rusin**. 2014. Sources of human-related injury and mortality for U.S. Pacific west coast marine mammal stock assessments: 2008-2012. NOAA Technical Memorandum, NOAA-TM-NMFS-SWFSC-533. [no abstract]

Wallace BP, **Schumacher J**, **Seminoff JA**, James MC. 2014. Biological and environmental influences on the trophic ecology of leatherback turtles in the northwest Atlantic. Marine Biology 161:1711–1724.

Abstract - Understanding the causes and consequences of variability in trophic status is important for interpreting population dynamics and for identifying important habitats for protected species like marine turtles. In the northwest atlantic Ocean, many leatherback turtles (Dermochelys coriacea) from distinct breeding stocks throughout the Wider caribbean region migrate to canadian waters sea- sonally to feed, but their trophic status during the migratory and breeding cycle and its implications have not yet been described. In this study, we used stable carbon and nitrogen isotope analyses of bulk skin to characterize the trophic status of leatherbacks in atlantic canadian waters by identify- ing trophic patterns among turtles and the factors influenc- ing those patterns. δ 15N values of adult males and females were significantly higher than those of turtles of unknown gender (i.e., presumed to be subadults), and δ15N increased significantly with body size. We found no significant dif- ferences among average stable isotope values of turtles according to breeding stock origin. Significant inter-annual variation in δ15N among cohorts probably reflects broad-scale oceanographic variability that drives fluctuations in stable isotope values of nutrient sources transferred through several trophic positions to leatherbacks, variation in base-line isotope values among different overwintering habitats used by leatherbacks, or a combination of both. Our results demonstrate that understanding effects of demographic and physiological factors, as well as oceanographic conditions, on trophic status is key to explaining observed patterns in population dynamics and for identifying important habitats for widely distributed, long-lived species like leatherbacks.

Week of 8 September 2014

Gorgone, A. M., **T. Eguchi**, B. L. Byrd, K. M. Altman, and A. A. Hohn. 2014. Estimating the abundance of the northern North Carolina estuarine system stock of common bottlenose dolphins (*Tursiops truncatus*). NOAA Technical Memorandum NMFS-SEFSC-664. 22p.

Abstract - The Northern North Carolina Estuarine System (NNCES) stock of the common bottlenose dolphin (*Tursiops truncatus*) has a small population size and low Potential Biological Removal level (PBR). Levels of serious injury and mortality due to commercial fisheries interactions may exceed the PBR. In addition, the prior abundance estimate, from a survey in 2006, is no longer valid for computing the PBR for the stock after 2014. To obtain a new abundance estimate, we conducted a capture-mark-recapture survey of the NNCES stock in the Pamlico-Albemarle Estuarine Complex (PAEC) from 15 June to 27 July 2013. The PAEC is the primary summer habitat for the stock. We surveyed 4,779 km of trackline, encountering 128 dolphin groups. We took

30,991 photographs, from which 471 individual dolphins were identified from distinctive nicks and notches on dorsal fins. Because dolphins in the most southern portion of the summer habitat overlap with the Southern North Carolina Estuarine System (SNCES) stock in July, some photographed dolphins could have been members of the SNCES stock. We developed a decision tree to identify dolphins that may have belonged to the SNCES stock, thereby allowing us to estimate abundance using all dolphins and then excluding those that might belong to the SNCES stock. We then calculated lower (823; 95% posterior interval (PI) = 733-931) and upper (873; 95% PI = 775-989) bounds on the abundance estimate based on habitat-use assumptions from the decision tree. Both estimates were obtained using closed capture-mark-recapture models and a novel method to correct for dolphins with indistinctive fins.

Pitman, R. L. 2014. One small catch. Natural History Magazine Sept:10-11. *No abstract*

Week of 25 August 2014

Leslie, M.S. 2014. Impacts of Phylogenetic Nomenclature on the Efficacy of the U.S. Endangered Species Act. Conservation Biology DOI: 10.1111/cobi.12375

Abstract - Cataloging biodiversity is critical to conservation efforts because accurate taxonomy is often a precondition for protection under laws designed for species conservation, such as the U.S. Endangered Species Act (ESA). Traditional nomenclatural codes governing the taxonomic process have recently come under scrutiny because taxon names are more closely linked to hierarchical ranks than to the taxa themselves. A new approach to naming biological groups, called phylogenetic nomenclature (PN), explicitly names taxa by defining their names in terms of ancestry and descent. PN has the potential to increase nomenclatural stability and decrease confusion induced by the rankbased codes. But proponents of PN have struggled with whether species and infraspecific taxa should be governed by the same rules as other taxa or should have special rules. Some proponents advocate the wholesale abandonment of rank labels (including species); this could have consequences for the implementation of taxon-based conservation legislation. I examined the principles of PN as embodied in the PhyloCode (an alternative to traditional rank-based nomenclature that names biological groups based on the results of phylogenetic analyses and does not associate taxa with ranks) and assessed how this novel approach to naming taxa might affect the implementation of species-based legislation by providing a case study of the ESA. The latest version of the PhyloCode relies on the traditional rank-based codes to name species and infraspecific taxa; thus, little will change regarding the main targets of the ESA because they will retain rank labels. For this reason, and because knowledge of evolutionary relationships

is of greater importance than nomenclatural procedures for initial protection of endangered taxa under the ESA, I conclude that PN under the PhyloCode will have little impact on implementation of the ESA.

Carretta, Oleson, Weller, Lang, Forney, Baker, Hanson, Martien, Muto, Orr, Huber, Lowry, Barlow, Lynch, Carswell, Brownell, and Matilla. 2013. U.S. Pacific Marine Mammal Stock Assessments, 2013. NOAA-TM-NMFS-SWFSC-532. Available at:

http://www.nmfs.noaa.gov/pr/sars/region.htm
no abstract

Week of 4 August 2014

Prosdocimi, L., **Dutton, P.H.**, Albareda, D., Remis, M. I. Origin and genetic diversity of leatherbacks (*Dermochelys coriacea*) at Argentine foraging grounds. *Journal of Experimental Marine Biology and Ecology* 458: 13–19. http://dx.doi.org/10.1016/j.jembe.2014.04.025 Abstract - To conduct conservation of migratory species, such as marine turtles, it is important to understand the population structure throughout the entire distribution of the species. We study the genetic composition of the leatherback turtles, *Dermochelys coriacea* foraging in waters off Argentina by analyzing 763 bp sequences of the mtDNA control region in order to determine the nesting origin of these animals. A total of 40 samples were collected from adult leatherbacks (mean 143.5; 180–123 cmcurved carapace length) captured (10%) in fisheries or encountered as strandings (90%). Based on analysis of mtDNA sequences we detected 4 haplotypes, the most common (n=26) being DC1.1, and the other rarer DC1.3 (n=4), DC13.1 (n=2), and DC1.4 (n=1). The genetic diversity was evaluated through the haplotype (0, 3712 \pm 0, 1000) and nucleotide diversities (0, 000521 \pm 0, 000553). Bayesian Mixed Stock Analysis (MSA) showed that the Buenos Aires foraging leatherbacks come primarily from the West African rookeries (Ghana and Gabon, mean estimate = 69% and 14% respectively). MSA results are consistent with those from mark–recapture studies, since four leatherbacks captured in Argentinean waters were adult females that were originally tagged on the nesting beaches in Gabon, West Africa. Our findings demonstrate the connection between nesting and foraging areas in the South Atlantic and illustrate the importance of the Malvinas ecoregion to the survival of migratory marine vertebrates, such as leatherbacks.

Curry, B. E. and Brownell, R. L., Jr. 2014. Family Balaenidae (Right and bowhead whales). Pages 186-213, *In*: Handbook of the Mammals of the World, volume 4, Sea Mammals, D. E. Wilson and R. A. Mittermeier, editors, Lynx Edicions, Barcelona 614 pp.

Abstract – no abstract.

Week of 14 July 2014

Eguchi, T. 2014 Estimating the proportion of identifiable individuals and group sizes in photographic identification studies. Marine Mammal Science 30:1120-1139.

Abstract - Simple Bayesian statistical models are introduced to estimate the proportion of identifiable individuals and group sizes in photographic identification, or photo-ID, studies of animals that are found in groups. The models require a simple random photographic sampling of animals, where the photographic captures are treated as sampling with replacement within each group. The total number of images, including those that cannot be identified, and the number of images that contain identifiable individuals are used to make inference about the proportion of identifiable individuals within each group and as the population when a number of groups are sampled. The numbers of images for individuals within each group are used to make inference about the group size. Based on analyses of simulated and real data, the models perform well with respect to accuracy and precision of posterior distributions of the parameters. Widths of posterior intervals were affected by the number of groups sampled, sampling duration, and the proportion of identifiable individuals in each group that was sampled. The structure of the models can accommodate covariates, which may affect photographic efficiency, defined in this study as the probability of photographically capturing individuals.

Week of 16 June 2014

Seminoff JA, Eguchi T, Carretta J, Allen C, Prosperi D, Rangel R, Gilpatrick J, Forney K, Peckham SH. 2014. Loggerhead sea turtle abundance at an offshore foraging hotspot in the eastern Pacific Ocean: implications for at-sea conservation. Endangered Species Research 24: 207–220.

Abstract - The Pacific Coast of the Baja California Peninsula (BCP), Mexico, is a hotspot for foraging loggerhead turtles *Caretta caretta* originating from nesting beaches in Japan. The BCP region is also known for anthropogenic sea turtle mortality that numbers thousands of turtles annually. To put the conservation implications of this mortality into biological context, we conducted aerial surveys to determine the distribution and abundance of loggerhead turtles in the Gulf of Ulloa, along the BCP Pacific Coast. Each year from 2005 to 2007, we surveyed ca. 3700 km

of transect lines, including areas up to 140 km offshore. During these surveys, we detected loggerhead turtles at the water's surface on 755 occasions (total of 785 loggerheads in groups of up to 7 turtles). We applied standard line-transect methods to estimate sea turtle abundance for survey data collected during good to excellent sighting conditions, which included 447 loggerhead sightings during ~6400 km of survey effort. We derived the proportion of time that loggerheads were at the surface and visible to surveyors based on in situ dive data. The mean annual abundance of 43 226 loggerhead turtles (CV = 0.51, 95 % CI range = 15 017 to 100 444) represents the first abundance estimate for foraging North Pacific loggerheads based on robust analytical approaches. Our density estimate confirms the importance of the BCP as a major foraging area for loggerhead turtles in the North Pacific. In the context of annual mortality estimates of loggerheads near BCP, these results suggest that up to 11% of the region's loggerhead population may perish each year due to anthropogenic and/or natural threats. We calculate that up to 50% of the loggerhead turtles residing in the BCP region in any given year will die within 15 yr if current mortality rates continue. This underscores the urgent need to minimize anthropogenic and natural mortality of local loggerheads.

Week of 26 May 2014

Martien, K.K., S.J. Chivers, R.W. Baird, F.I. Archer, A.M. Gorgone, B.L. Hancock-Hanser, D. Mattila, D.J. McSweeney, E.M. Oleson, C. Palmer, V.L. Pease, K.M. Robertson, G.S. Schorr, M.B. Schultz, D.L. Webster, B.L. Taylor. 2014. Nuclear and mitochondrial patterns of population structure in North Pacific false killer whales (*Pseudorca crassidens*). Journal of Heredity. doi: 10.1093/jhered/esu029.

Abstract - False killer whales (*Pseudorca crassidens*) are large Delphinids typically found in deep water far offshore. However, in the Hawaiian Archipelago there are two resident island-associated populations of false killer whales, one in the waters around the main Hawaiian Islands (MHI) and one in the waters around the Northwestern Hawaiian Islands (NWHI). We use mitochondrial DNA (mtDNA) control region sequences and genotypes from 16 nuclear (nucDNA) microsatellite loci from 206 individuals to examine levels of differentiation among the two island-associated populations and offshore animals from the central and eastern North Pacific. Both mtDNA and nucDNA exhibit highly significant differentiation between populations, confirming limited gene flow in both sexes. The mtDNA haplotypes exhibit a strong pattern of phylogeographic concordance, with island-associated populations sharing three closely related haplotypes not found elsewhere in the Pacific. However, nucDNA data suggests that NWHI animals are at least as differentiated from MHI animals as they are from offshore animals. The patterns of differentiation revealed by the two marker types suggest that the island-associated false killer whale populations likely share a common colonization history, but have limited contemporary gene flow.

Urian, Kim, Antoinette Gorgone, Andrew Read, Brian Balmer, Randall S. Wells, Per Berggren, **John Durban, Tomoharu Eguchi**, William Rayment, and Philip S. Hammond. 2014. Recommendations for photo-identification methods used in capture-recapture models with cetaceans. Marine Mammal Science.

Abstract - Capture-recapture methods are frequently employed to estimate abundance of cetaceans using photographic techniques and a variety of statistical models. However, there are many unresolved issues regarding the selection and manipulation of images that can potentially impose bias on resulting estimates. To examine the potential impact of these issues we circulated a test data set of dorsal fin images from bottlenose dolphins to several independent research groups. Photo-identification methods were generally similar, but the selection, scoring, and matching of images varied greatly amongst groups. Based on these results we make the following recommendations. Researchers should: (1) determine the degree of marking, or level of distinctiveness, and use images of sufficient quality to recognize animals of that level of distinctiveness; (2) ensure that markings are sufficiently distinct to eliminate the potential for "twins" to occur; (3) stratify data sets by distinctiveness and generate a series of abundance estimates to investigate the influence of including animals of varying degrees of markings; and (4) strive to examine and incorporate variability among analysts into capture-recapture estimation. In this paper we summarize these potential sources of bias and provide recommendations for best practices for using natural markings in a capture-recapture framework.

Week of 05 May 2014

Connie Ka-yan Ng, **Peter H. Dutton**, Simon Kin-fung Chan, Ka-shing Cheung, Jian-wen Qiu, and Yanan Sun. (2014) Characterization and Conservation Concerns of Green Turtles (*Chelonia mydas*) Nesting in Hong Kong, China. Pacific Science, 68(2):231-243.

Abstract - Hong Kong has one of the last remaining nesting populations of endangered green turtles (Chelonia mydas) in southern China. Because nesting individuals are vital to sustain populations, this study characterizes and reports essential baseline information about nesting pattern, postnesting movement, and genetic composition of green turtles nesting in Hong Kong to provide a basis for effective scientific-based management of this migratory species. The number of nesters observed in Hong Kong was relatively low compared with other rookeries in southern China, but the nesting pattern in terms of clutch size and interesting interval was comparable with that of other nearby rookeries. These nesters are likely a remnant of a small population previously depleted as a result of historical harvesting of eggs in Hong Kong. Based on available DNA sequences and literature, we identified two mtDNA haplotypes, CmP18 (which is also common in the rookery in Taiwan) and a novel endemic haplotype (CmP116). We found significant differentiation based on haplotype frequencies between populations in Hong Kong and Lanyu, Taiwan, indicating that these nesting populations are demographically isolated. Loss of these populations would therefore result in loss of genetic diversity for this species in the region. Satellite tracking of the local nesters revealed postnesting movement to foraging habitats in Vietnam and Hainan Island. International cooperation

Week of 28 April 2014

green turtle assemblages in the region.

Ballance, L.T., Barre, Bengtson, Bettridge, Bisack, Brown, Fahy, Ford, Garrison, LeBoeuf, **R. LeRoux**, Parrish, Seney, Simpkins, Srinivasan, VanAtta, Vardi. 2014. NOAA's National Marine Fisheries Service Protected Resources Science Investment and Planning Process (PRSIPP): highlights and significant outcomes of the September 2013 steering committee meeting. NOAA Technical Memorandum NMFS-F/SPO-140.

and consistent dedicated research are of paramount importance to conservation and recovery of

No abstract

Week of 21 April 2014

Tucker AD, MacDonald BD, Seminoff JA. 2014. Foraging site fidelity and stable isotope values of loggerhead turtles tracked in the Gulf of Mexico and northwest Caribbean. Marine Ecology Progress Series 502: 267–279. Abstract - We used stable isotope (δ 13C, δ 15N, δ 34S) analysis in combination with satellite telemetry to evaluate the foraging areas chosen by 88 loggerhead turtles Caretta caretta nesting in southwestern Florida. Nine turtles were tracked and skin-sampled in more than one nesting season to evaluate within-individual consistency in foraging sites and stable isotope values. Turtles migrated to 5 regions: Caribbean, Florida Keys, West Florida Shelf, northern Gulf of Mexico, and Yucatan Peninsula. The stable isotope ratios across these foraging grounds ranged from -21.16 to -7.69 % for $\delta13$ C, 3.27 to 13.99 % for $\delta15$ N, and 1.91 to 20.64 ‰ for δ34S. We compared bulk skin tissue stable isotope values for all turtles by bioregion, year, body size, depth of putative foraging area, and linear distance from the closest shore; among these factors, only bioregion showed a significant effect on isotope values. There were subtle regional differences in mean δ13C, δ15N, and δ34S, and an apparent north-south isotopic shift aligning strongly with ocean currents adjacent to the Florida Keys. The influence of coastal topography and shifting biogeographic boundaries such as the Loop Current may cause strong ocean water mixing that results in the observed similarities in stable isotope values among regions. These results indicate that stable isotopes alone may be an inadequate tool for identifying fine-scale (<100 km) residency of sea turtles within this ocean region.

Week of 14 April 2014

Carretta, J.V., L. Enriquez, and C. Villafana. 2014. Marine mammal, sea turtle, and seabird bycatch in California gillnet fisheries in 2012. NOAA Technical Memorandum SWFSC-TM-526.

Overview - Bycatch of marine mammals, sea turtles, and seabirds is reported for two gillnet fisheries in 2012: 1) the California (CA) swordfish and thresher shark drift gillnet fishery, and 2) the CA halibut and white seabass set gillnet fishery, based on fishery observer data collected in 2012. Bycatch estimates are generated using ratio estimation methods. Observations in the CA swordfish and thresher shark drift gillnet fishery included 83 sets during 15 fishing trips, from an estimated 445 sets fished by all vessels (18.7% observer coverage). Observed bycatch included 5 short-beaked common dolphins (*Delphinus delphis*), one northern right whale dolphin (*Lissodelphis borealis*), and six California sea lions (*Zalophus californianus*). Additionally, one leatherback sea turtle (*Dermochelys coriacea*) was reported released alive and we provide an estimate of entanglements of this species in 2012. Estimated bycatch is 26 (CV=0.78) short-beaked common dolphins, five (CV=1.01) northern right whale dolphins, and 32 (CV=0.60) California sea lions. The estimated number of leatherback turtle entanglements in 2012 is five (CV=1.09), based on the observation of one entangled turtle and 18.7% observer coverage.

Observations in the CA halibut and white seabass set gillnet fishery included 75 days of fishing, from an estimated 1,360 days fished by all vessels (5.5% observer coverage). Observed bycatch included 18 California sea lions, one pelagic cormorant (*Phalacrocorax pelagicus*), and three unidentified cormorants (*Phalacrocorax* sp). Estimated bycatch is 326 (CV=0.33) California sea lions, 18 (CV=0.98) pelagic cormorants and 54 (CV=0.72) unidentified cormorants. Two additional fisheries observed in 2012 did not have any recorded bycatch of marine mammals, seabirds, or sea turtles. The CA yellowtail, barracuda, and white seabass drift gillnet fishery had very low observer coverage, with three observed sets during one fishing trip, from an estimated 141 trips fished (0.7% observer coverage). The CA pelagic longline fishery, which operates outside of the U.S. Exclusive Economic Zone, was also observed in 2012, with 100% observer coverage and no observed bycatch.

Keating, J. L., Barlow, J., and Rankin, S. 2014. Cruise report for passive acoustic monitoring component of the 2013 SOCAL-Behavioral Response Study. NOAA Administrative Report. LJ-14-01. *No Abstract*

Week of 7 April 2014

De Beukelaer, S., Miller, C., Moore, T.J., Kathey, S., and Grimmer K.. 2014. Monterey Bay National Marine Sanctuary Vessel Traffic Analysis 2009-2012. Monterey Bay National Marine Sanctuary Technical Report, 44 pp. Executive Summary - Monterey Bay National Marine Sanctuary (MBNMS) staff and stakeholders sought to have a better understanding of vessel compliance with the International Maritime Organization (IMO) recommended tracks within the MBNMS that were established in 2000. Three different analyses using Automated Information System (AIS) ship traffic data were completed to address this question. The Naval Postgraduate School (NPS) reviewed daily AIS data from September 2009-2012 and found that annually less than 8 individual cargo vessels deviated more than 3 nautical miles inshore of the northbound recommended track for vessels 300 gross tons and above and only one tanker was found deviating from that northbound track in that time-period. A further refinement of the analysis of the tanker traffic would be facilitated by access to data on the association and contents of each vessel because Western States Petroleum Association (WSPA) tankers carry crude oil, black oil, or other persistent liquid cargo in bulk and have agreed to stay more than 50 nautical miles offshore. The Southwest Fisheries Science Center of the National Marine Fisheries Service completed density maps for 2009 AIS data and found that tankers are using the recommended tracks, particularly those designated for vessels carrying hazardous cargo in bulk with an especially higher density using the southbound track. The 2009 data analysis by the Southwest Fisheries Science Center indicated higher densities of cargo vessels in the northbound recommended track for vessels 300 gross tons and above than in the other three tracks. MBNMS began conducting random daily reviews of AIS data on October 1, 2012 and staff contact the United States Coast Guard (USCG) when a deviation of more than 3 nautical miles inshore of the northbound recommended track for vessels 300 gross tons and above is noted. The USCG verifies the AIS data and contacts the vessel if they determine that the AIS data do reflect a deviation. These three

AIS analyses do indicate that a great majority of the vessels that transit through the MBNMS are complying with the IMO recommended tracks.

Week of 31 March 2014

Mark S. Lowry, Richard Condit, Brian Hatfield, Sarah G. Allen, Ryan Berger, Patricia A. Morris, Burney J. Le Boeuf, and J. Reiter. 2014. Abundance, Distribution, and Population Growth of the Northern Elephant Seal (*Mirounga angustirostris*) in the United States from 1991 to 2010. Aquatic Mammals 2014, 40(1), 20-31, DOI 10.1578/AM.40.1.2014.20

Abstract - We report on the distribution and abundance of the northern elephant seal (Mirounga angustirostris) in the United States from 1991 to 2010. Pup production (i.e., births) was the principal metric used to characterize abundance, distribution, and population growth of the U.S. population and of each rookery in the U.S. Birth estimates were obtained from the literature and estimated from recent counts of adult females or counts of pups made during ground and aerial photographic surveys conducted during the pupping-breeding season at all rookeries in central California and the Channel Islands in southern California. A total of 40,684 pups were estimated to have been born at 11 rookeries in the U.S. in 2010. The two most productive rookeries as of 2010 were San Miguel Island (16,208 pups) and San Nicolas Island (10,882 pups). The Piedras Blancas rookery was not established in 1991 but has since grown to be the fourth largest rookery as of 2010. Rookeries grew most rapidly initially, presumably due to high immigration rates; then increased moderately, eventually becoming stable; and some declined in size. Since 1988, the U.S. population has been growing at an average annual rate of 3.8%. The multiplicative factor needed to estimate total population size from pup production is estimated at 4.4. Total U.S. population size in 2010 was estimated at 179,000 individuals. Using conservative estimates for population growth of northern elephant seals in Mexico, we estimate that the total population in Mexico and the U.S. in 2010 was between 210,000 and 239,000 individuals.

Week of 24 March 2014

Rebecca L. Lewison, Larry B. Crowder, Bryan P. Wallace, **Jeffrey E. Moore**, Tara Cox, Ramunas Zydelis, Sara McDonald, Andrew DiMatteo, Daniel C. Dunn, Connie Y. Kot, Rhema Bjorkland, Shaleyla Kelez, Candan Soykan, **Kelly R. Stewart**, Michelle Sims, Andre Boustany, Andrew J. Read, Patrick Halpin, W. J. Nichols, and Carl Safina. 2014. Global patterns of marine mammal, seabird, and sea turtle bycatch reveal taxa-specific and cumulative megafauna hotspots. Proceedings of the National Academy of Sciences of the United States of America. doi: 10.1073/pnas.1318960111

Abstract - Recent research on ocean health has found large predator abundance to be a key element of ocean condition. Fisheries can impact large predator abundance directly through targeted capture and indirectly through incidental capture of nontarget species or bycatch. However, measures of the global nature of bycatch are lacking for air-breathing megafauna. We fill this knowledge gap and present a synoptic global assessment of the distribution and intensity of bycatch of seabirds, marine mammals, and sea turtles based on empirical data from the three most commonly used types of fishing gears worldwide. We identify taxaspecific hotspots of bycatch intensity and find evidence of cumulative impacts across fishing fleets and gears. This global map of bycatch illustrates where data are particularly scarce—in coastal and small-scale fisheries and ocean regions that support developed industrial fisheries and millions of small-scale fishers—and identifies fishing areas where, given the evidence of cumulative hotspots across gear and taxa, traditional species or gear-specific bycatch management and mitigation efforts may be necessary but not sufficient. Given the global distribution of bycatch and the mitigation success achieved by some fleets, the reduction of air-breathing megafauna bycatch is both an urgent and achievable conservation priority.

Week of 17 March 2014

Miller, B. S., K. Collins, J. **Barlow**, S. Calderan, R. Leaper, M. McDonald, P. Ensor, P. A. **Olson**, C. Olavarria, and M. C. Double. 2014. Blue whale vocalizations recorded around New Zealand: 1964-2013. Journal Acoustical Society of America 135(3):1616-1623.

Abstract - Previous underwater recordings made in New Zealand have identified a complex sequence of low

frequency sounds that have been attributed to blue whales based on similarity to blue whale songs in other areas. Recordings of sounds with these characteristics were made opportunistically during the Southern Ocean Research Partnership's recent Antarctic Blue Whale Voyage. Detections of these sounds occurred all around the South Island of New Zealand during the voyage transits from Nelson, New Zealand to the Antarctic and return. By following acoustic bearings from directional sonobuoys, blue whales were visually detected and confirmed as the source of these sounds. These recordings, together with the historical recordings made northeast of New Zealand, indicate song types that persist over several decades and are indicative of the year-round presence of a population of blue whales that inhabits the waters around New Zealand. Measurements of the four-part vocalizations reveal that blue whale song in this region has changed slowly, but consistently over the past 50 years. The most intense units of these calls were detected as far south as 53°S, which represents a considerable range extension compared to the limited prior data on the spatial distribution of this population.

Week of 10 March 2014

Bradford AL, **Forney** KA, Oleson EM, and **Barlow** J (2014) Accounting for Subgroup Structure in Line-Transect Abundance Estimates of False Killer Whales (*Pseudorca crassidens*) in Hawaiian Waters. PLoS ONE 9(2): e90464. doi:10.1371/journal.pone.0090464

http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0090464

Abstract - For biological populations that form aggregations (or clusters) of individuals, cluster size is an important parameter in line-transect abundance estimation and should be accurately measured. Cluster size in cetaceans has traditionally been represented as the total number of individuals in a group, but group size may be underestimated if group members are spatially diffuse. Groups of false killer whales (*Pseudorca* crassidens) can comprise numerous subgroups that are dispersed over tens of kilometers, leading to a spatial mismatch between a detected group and the theoretical framework of line-transect analysis. Three stocks of false killer whales are found within the U.S. Exclusive Economic Zone of the Hawaiian Islands (Hawaiian EEZ): an insular main Hawaiian Islands stock, a pelagic stock, and a Northwestern Hawaiian Islands (NWHI) stock. A ship-based line-transect survey of the Hawaiian EEZ was conducted in the summer and fall of 2010, resulting in six systematic-effort visual sightings of pelagic (n = 5) and NWHI (n = 1) false killer whale groups. The maximum number and spatial extent of subgroups per sighting was 18 subgroups and 35 km, respectively. These sightings were combined with data from similar previous surveys and analyzed within the conventional line-transect estimation framework. The detection function, mean cluster size, and encounter rate were estimated separately to appropriately incorporate data collected using different methods. Unlike previous line-transect analyses of cetaceans, subgroups were treated as the analytical cluster instead of groups because subgroups better conform to the specifications of line-transect theory. Bootstrap values (n = 5,000) of the line-transect parameters were randomly combined to estimate the variance of stock-specific abundance estimates. Hawai'i pelagic and NWHI false killer whales were estimated to number 1,552 (CV = 0.66; 95% CI = 479–5,030) and 552 (CV = 1.09; 95% CI = 97–3,123) individuals, respectively. Subgroup structure is an important factor to consider in line-transect analyses of false killer whales and other species with complex grouping patterns.

Week of 3 March 2014

Ehlers, Libby P.W., Chris J. Johnson and Dale R. Seip. 2014. Movement ecology of wolves across an industrial landscape supporting threatened populations of woodland caribou. Landscape Ecology 29(3):451-465.

Abstract - Woodland caribou (Rangifer tarandus caribou) are a species of increasing conservation concern across North America. Throughout much of boreal Canada, human developments, including forestry and energy development, are now accepted causes of the decline in the number and distribution of caribou. One of the hypothesised mechanisms for the decline is altered predator—prey dynamics. We quantified the impacts of a variety of industrial activities on gray wolf (Canis lupus) and caribou interactions at a regional scale. We used animal locations collected with global positioning system collars and field data to examine how a range of industrial developments influenced the movements of wolves. We quantified the speed of wolf movements and the tortuosity of movement paths at two spatiotemporal scales across forested boreal and mountainous environments occupied by woodland caribou. Habitat and disturbance features better explained wolf

movements during the weekly scale. In general, linear movements increased during winter, which paralleled past studies that suggested linear travel by wolves was associated with deep snow and the increased maintenance and patrol of territories. Wolves decreased movement rates but not sinuosity within close proximity to disturbance features, thus implying behaviours near such features were more closely associated with prey searching and hunting. Alternatively, wolves increased movement rates and linear travel through areas with high densities of linear and non-linear industrial features; this response suggested that wolves avoided spending time in high-risk areas associated with human activities. Results of this study further our understanding of wolf distribution and behaviour in habitats supporting populations of caribou within a matrix of industrial developments.

Week of 24 February 2014

Rebecca L. Lewison, Larry B. Crowder, Bryan Wallace, **Jeff Moore**, Tara Cox, Ramunas Zydelis, Sara McDonald, Andrew DiMatteo, Daniel Dunn, Connie Y. Kot, Rhema Bjorkland, Shaleyla Kelez, Candan Soykan, **Kelly R. Stewart**, Michelle Sims, Andre Boustany, Andrew J. Read, Pat Halpin, W.J. Nichols, Carl Safina. *In Press*. Global patterns of seabird, marine mammal, and sea turtle bycatch reveal taxa-specific and cumulative megafauna hotspots. Proc. Nat. Acad. of Sciences.

Abstract - Recent research on ocean health has found large predator abundance to be a key element of ocean condition. Fisheries can impact large predator abundance directly through targeted capture and indirectly through incidental capture of non-target species, or bycatch. However, measures of the global nature of bycatch are lacking for air-breathing megafauna. We fill this knowledge gap and present the first global assessment of the distribution and intensity of bycatch of seabirds, marine mammals, and sea turtles based on empirical data from the three most commonly used types of fishing gears worldwide. We identify taxaspecific hotspots of bycatch intensity and find evidence of cumulative impacts across fishing fleets and gears. This global map of bycatch illustrates where data are particularly scarce - in coastal and small-scale fisheries and in ocean regions that support developed industrial fisheries and millions of small-scale fishers – and identify fishing areas where, given the evidence of cumulative hotspots across gear and taxa, traditional species or gear-specific bycatch management and mitigation efforts may be necessary, but not sufficient. Given the global distribution of bycatch and the mitigation success achieved by some fleets, the reduction of air-breathing megafauna bycatch is both an urgent and achievable conservation priority.

Week of 10 February 2014

Merel L. Dalebout, C. Scott Baker, Debbie Steel, Kirsten Thompson, **Kelly M. Robertson, Susan J. Chivers, William F. Perrin**, Smanori Goonatilake, Charles Anderson, James G. Meadand Charles W. Potter, Lisa Thompson, Danielle Jupiter and Tadasu K. Yamada. 2014. Resurrection of *Mesoplodon hotaula Deraniyagala* 1963: A new species of beaked whale in the tropical Indo-Pacific. Marine Mammal Science doi 10.1111/mms.12113.

Abstract - We present genetic and morphological evidence supporting the recognition of a previously synonymized species of *Mesoplodon* beaked whale in the tropical Indo-Pacific, *Mesoplodon hotaula*. Although the new species is closely-related to the rare ginkgo-toothed beaked whale *M. ginkgodens*, we show that these two lineages can be differentiated by maternally (mitochondrial DNA), biparentally (autosomal), and paternally (Y chromosome) inherited DNA sequences, as well as by morphological features. The reciprocal monophyly of the mtDNA genealogies and the largely parapatric distribution of these lineages is consistent with reproductive isolation. The new lineage is currently known from at least seven specimens: Sri Lanka (1), Gilbert Islands, Republic of Kiribati (1+), Palmyra Atoll, Northern Line Islands,

U.S.A. (3), Maldives (1), and Seychelles (1). The type specimen (Sri Lanka) was described as a new species, *M. hotaula*, in 1963, but later synonymized with *M. ginkgodens*. This discovery brings the total number of *Mesoplodon* species to 15, making it, by far, the most speciose yet least known genus of cetaceans.

Sara Keen, Jesse C. Ross, **Emily T. Griffiths**, Michael Lanzone, and Andrew Farnsworth. 2014. A comparison of similarity-based approaches in the classification of flight calls of four species of North American wood-warblers (Parulidae). Ecological Informatics. http://dx.doi.org/10.1016/j.ecoinf.2014.01.001

Abstract: Numerous methods are available for analysis of avian vocalizations, but few research efforts have compared recent methods for calculating and evaluating similarity among calls, particularly those collected in the field. This manuscript compares a suite of methodologies for analyzing flight calls of New World warblers, investigating the effectiveness of four techniques for calculating call similarity: (1) spectrographic cross-correlation, (2) dynamic time warping, (3) Euclidean distance between spectrogram-based feature measurements, and (4) random forest distance between spectrogram-based feature measurements. We tested these methods on flight calls, which are short, structurally simple vocalizations typically used during nocturnal migration, as these signals may contain important ecological or demographic information. Using the four techniques listed above, we classified flight calls from three datasets, one collected from captive birds and two collected from wild birds in the field. Each dataset contained an equal number of calls from four warbler species commonly recorded during acoustic monitoring: American Redstart, Chestnut-sided Warbler, Hooded Warbler, and Ovenbird. Using captive recordings to train the classification models, we created four similarity-based classifiers which were then tested on the captive and field datasets. We show that these classification methods are limited in their ability to successfully classify the calls of these warbler species, and that classification accuracy was lower on field recordings than captive recordings for each of the tested methods. Of the four methods we compared, the random forest technique had the highest classification accuracy, enabling correct classification of 67.6% of field recordings. To compare the performance of the automated techniques to manual classification, the most common method used in flight call research, human experts were also asked to classify calls from each dataset. The experts correctly classified approximately 90% of field recordings, indicating that although the automated techniques are faster, they remain less accurate than manual classification. However, because of the challenges inherent to these data, such as the structural similarity among the flight calls of focal species and the presence of environmental noise in the field recordings, some of the tested automated classification techniques may be acceptable for real-world applications. We believe that this comparison of broadly applicable methodologies provides information that will prove to be useful for analysis, detection and classification of short duration signals. Based on our results, we recommend that a combination of feature measurements and random forest classification can be used to assign flight calls to species, while human experts oversee the process.

Week of 3 February 2014

Elizabeth A. Becker, **Karin A. Forney**, David G. Foley, Raymond C. Smith, **Thomas J. Moore**, **Jay Barlow**. 2014. Predicting seasonal density patterns of California cetaceans based on habitat models. Endangered Species Research Vol. 23: 1–22, doi: 10.3354/esr00548

Abstract - Temporal variability in species distribution remains a major source of uncertainty in managing protected marine species, particularly in ecosystems with significant seasonal or interannual variation, such as the California Current Ecosystem (CCE). Spatially explicit species-habitat models have become valuable tools for decision-makers assisting in the development and implementation of measures to reduce adverse impacts (e.g., from fishery bycatch, ship strikes, anthropogenic sound), but such models are often not available for all seasons of interest. Broad-scale migratory patterns of many of the large whale species are well-known, while seasonal distribution shifts of small cetaceans are typically less well understood. Within the CCE, species-habitat models have been developed based on six summer-fall surveys conducted during 1991-2008. In this study, we evaluate whether the between-year oceanographic variability can inform species predictions during winter-spring periods. Generalized additive models were developed to predict abundance of four cetacean species/genera known to have year-round occurrence in the CCE: common dolphins (Delphinus spp.), Pacific white-sided dolphin (Lagenorhynchus obliquidens), northern right whale dolphin (Lissodelphis borealis), and Dall's porpoise (Phocoenoides dalli). Predictor variables included a combination of temporally dynamic, remotely sensed environmental variables and geographically fixed variables. Acrossseason predictive ability was evaluated relative to aerial surveys conducted in winter-spring 1991-92, using observed:predicted density ratios, nonparametric Spearman rank correlation tests, and visual inspection of predicted and observed distributions by species. Seasonal geographic patterns of species density were captured effectively for most species, although some model limitations were evident, particularly when the original summer-fall data did not adequately capture winter-spring habitat conditions.

Hawaii and American Samoa Longline Fisheries during 2007-2011. U.S. Dep. Commer., NOAA Tech. Memo., NOAA-TM-NMFS-PIFSC-39, 20 p. + Appendix

Abstract - Cetacean interactions (i.e., hookings and entanglements) with the Hawaii and American Samoa longline fisheries observed during 2007-2011 were compiled, and the number of cetacean deaths, serious injuries, and non-serious injuries by fishery, species, and management area were assessed. These values form the basis of the mortality and serious injury estimates included in the stock assessment reports of stocks impacted by these fisheries. Injury determinations were made using a revised process for distinguishing serious from non-serious injuries (National Marine Fisheries Service, 2012). In the Hawaii deep-set fishery, 50 cetacean interactions were observed from 2007 to 2011; most involved false killer whales (48.0%),

resulted in death or serious injury (73.5%), and occurred outside the U.S. exclusive economic zone, or EEZ (54.0%). In the Hawaii shallow-set fishery, 46 cetacean interactions were observed from 2007 to 2011; most involved Risso's dolphins (45.7%), resulted in death or serious injury (77.2%), and occurred outside the U.S. EEZ (91.3%). In the American Samoa deep-set fishery, 14 cetacean interactions were observed from 2007 to 2011; most involved rough-toothed dolphins (42.9%), resulted in death or serious injury (92.9%), and occurred within the U.S. EEZ (85.7%).

Frey A, Dutton PH, Shaver DJ, Walker JS, Rubio C (2014) Kemp's ridley (*Lepidochelys kempii*) nesting abundance in Texas: a novel approach using genetics to improve population census. Endangered Species Research 23: 63–71, 2014 doi: 10.3354/esr00565.

Abstract - Accurate estimates of the annual numbers of nesting females are critical for assessing sea turtle populations. There has been a significant increase in nesting by Kemp's ridley (*Lepidochelys kempii*) turtles at Padre Island National Seashore (PAIS) and nearby beaches in Texas, USA. There were 4 nests observed in Texas during 1995 and a record of 209 in 2012. However, it is unclear how many clutches are laid by the same female turtles. We use a genetic approach to infer the number of individual nesters from genotypes determined from dead embryos and hatchlings sampled from clutches. Mitochondrial DNA sequencing was combined with nuclear DNA analysis at 10 microsatellite loci to match genotypes for nesters and offspring of unknown parentage in over 50% of the unassigned nests. Our results indicate that traditional methods, based on observed tagged turtles, have underestimated the number of Kemp's ridleys nesting in Texas. We demonstrate how genetic approaches can be incorporated into population assessments when direct census of adult animals is not feasible. This approach also provides a basis to apply Capture-Mark-Recapture techniques to impact assessment of events, such as the recent oil spill, on the population via sampling of nests to identify and track individual nesters over time.

Naro-Maciel, E., Gaughran, S.J., Putman, N.F., Amato, G., Arengo, F., **Dutton, P.H.**, McFadden, K.W., Vintinner, E.C., Sterling, E.J. (2014) Predicting connectivity of green turtles at Palmyra Atoll, Central Pacific: A focus on mtDNA and dispersal modeling. Journal of the Royal Society Interface 11, 20130888.

Abstract - Population connectivity and spatial distribution are fundamentally related to ecology, evolution, and behavior. Here we combined powerful genetic analysis with high quality simulations of particle dispersal in an ocean circulation model to investigate the distribution of green turtles foraging at the remote Palmyra Atoll National Wildlife Refuge, Central Pacific. We analyzed mitochondrial sequences from turtles (n = 349) collected there over five years (2008 - 2012). Genetic analysis assigned natal origins almost exclusively (~97%) to the West Central and South Central Pacific combined Regional Management Units. Further, our modeling results indicated that turtles could potentially drift to Palmyra Atoll via surface currents along a near-Equatorial swathe traversing the Pacific. Comparing findings from genetics and modeling highlighted the complex impacts of ocean currents and behavior on natal origins. Although the Palmyra feeding ground was highly differentiated genetically from others in the Indo-Pacific, there was no significant differentiation among years, sexes, or stage-classes at the Refuge. Understanding the population distribution of this foraging population advances knowledge of green turtles and contributes to effective conservation planning for this threatened species.

Week of 27 January 2014

Simone Baumann-Pickering, Marie A. Roch, **Robert L. Brownell Jr.**, Anne E. Simonis, Mark A. McDonald, Alba Solsona-Berga, Erin M. Oleson, Sean M. Wiggins, John A. Hildebrand. 2014. Spatio-Temporal Patterns of Beaked

Whale Echolocation Signals in the North Pacific. PLOS ONE 9(1): e86072. doi:10.1371/journal.pone.0086072 Abstract - At least ten species of beaked whales inhabit the North Pacific, but little is known about their abundance, ecology, and behavior, as they are elusive and difficult to distinguish visually at sea. Six of these species produce known species-specific frequency modulated (FM) echolocation pulses: Baird's, Blainville's, Cuvier's, Deraniyagala's, Longman's, and Steineger's beaked whales. Additionally, one described FM pulse (BWC) from Cross Seamount, Hawai'i, and three unknown FM pulse types (BW40, BW43, BW70) have been identified from almost 11 cumulative years of autonomous recordings at 24 sites throughout the North Pacific. Most sites had a dominant FM pulse type with other types being either absent or limited. There was not a strong seasonal influence on the occurrence of these signals at any site, but longer time series may reveal smaller, consistent fluctuations. Only the species producing BWC signals, detected throughout the Pacific Islands region, consistently showed a diel cycle with nocturnal foraging. By comparing stranding and sighting information with acoustic findings, we hypothesize that BWC signals are produced by ginkgo-toothed beaked whales. BW43 signal encounters were restricted to Southern California and may be produced by Perrin's beaked whale, known only from Californian waters. BW70 signals were detected in the southern Gulf of California, which is prime habitat for Pygmy beaked whales. Hubb's beaked whale may have produced the BW40 signals encountered off central and southern California; however, these signals were also recorded off Pearl and Hermes Reef and Wake Atoll, which are well south of their known range.

Roe JH, Morreale SJ, Paladino FV, Shillinger GJ, Benson SR, Eckert SA, Bailey H, Santidrian-Tomillo P, Bograd SJ, **Eguchi T, Dutton PH, Seminoff JA**, Block BA, Spotila JR (2014) Predicting bycatch hotspots for endangered leatherback turtles on longlines in the Pacific Ocean. Proceedings of the Royal Society B. doi.org/10.1098/rspb.2013.2559

Abstract - Fisheries bycatch is a critical source of mortality for rapidly declining populations of leatherback turtles, Dermochelys coriacea. We integrated use-intensity distributions for 135 satellite-tracked adult turtles with longline fishing effort to estimate predicted bycatch risk over space and time in the Pacific Ocean. Areas of predicted bycatch risk did not overlap for eastern and western Pacific nesting populations, warranting their consideration as distinct management units with respect to fisheries bycatch. For western Pacific nesting populations, we identified several areas of high risk in the north and central Pacific, but greatest risk was adjacent to primary nesting beaches in tropical seas of Indo-Pacific islands, largely confined to several exclusive economic zones under the jurisdiction of national authorities. For eastern Pacific nesting populations, we identified moderate risk associated with migrations to nesting beaches, but the greatest risk was in the South Pacific Gyre, a broad pelagic zone outside national waters where management is currently lacking and may prove difficult to implement. Efforts should focus on these predicted hotspots to develop more targeted management approaches to alleviate leatherback bycatch.

Shamblin BM, Bolten AB, Abreu-Grobois FA, Bjorndal KA, Cardona L, et al. incl. **Dutton, P**. 2014. Geographic Patterns of Genetic Variation in a Broadly Distributed Marine Vertebrate: New Insights into Loggerhead Turtle Stock Structure from Expanded Mitochondrial DNA Sequences. PLoS ONE 9(1): e85956. doi:10.1371/journal.pone.0085956

Abstract - Previous genetic studies have demonstrated that natal homing shapes the stock structure of marine turtle nesting populations. However, widespread sharing of common haplotypes based on short segments of the mitochondrial control region often limits resolution of the demographic connectivity of populations. Recent studies employing longer control region sequences to resolve haplotype sharing have focused on regional assessments of genetic structure and phylogeography. Here we synthesize available control region sequences for loggerhead turtles from the Mediterranean Sea, Atlantic, and western Indian Ocean basins. These data represent six of the nine globally significant regional management units (RMUs) for the species and include novel sequence data from Brazil, Cape Verde, South Africa and Oman. Genetic tests of differentiation among 42 rookeries represented by short sequences (380 bp haplotypes from 3,486 samples) and 40 rookeries represented by long sequences (,800 bp haplotypes from 3,434 samples) supported the distinction of the six RMUs analyzed as well as recognition of at least 18 demographically independent management units (MUs) with respect to female natal homing. A total of 59 haplotypes were resolved. These haplotypes belonged to two highly divergent global lineages, with haplogroup I represented primarily by CC-A1, CC-A4, and CC-A11 variants and haplogroup II represented by CC-A2 and derived variants. Geographic

distribution patterns of haplogroup II haplotypes and the nested position of CCA11.6 from Oman among the Atlantic haplotypes invoke recent colonization of the Indian Ocean from the Atlantic for both global lineages. The haplotypes we confirmed for western Indian Ocean RMUs allow reinterpretation of previous mixed stock analysis and further suggest that contemporary migratory connectivity between the Indian and Atlantic Oceans occurs on a broader scale than previously hypothesized. This study represents a valuable model for conducting comprehensive international cooperative data management and research in marine ecology.

JORGE TORRE, OMAR VIDAL, and **ROBERT L. BROWNELL, JR**. 2014. Sexual dimorphism and developmental patterns in the external morphology of the vaquita, *Phocoena sinus*. Marine Mammal Science DOI: 10.1111/mms.12106

Abstract - A total of 56 vaquitas (*Phocoena sinus*) were examined to evaluate their sexual dimorphism and isometric and/or allometric growth in 35 external characteristics. Absolute and relative (to total length) measurements and growth rates were compared between sexually immature and mature females and males. T-tests and analysis of variance (ANOVA) and covariance (ANCOVA) were used to evaluate sexual dimorphism. Sexual dimorphism in the vaquita was detected in the total length, head region (from blowhole to tip of upper jaw), anterior section of the body (from dorsal fin to tip of upper jaw), dorsal fin and the genital and anal regions. Fluke width is relatively larger in mature males than immature males, but in females this relative metric does not change during their development. In addition, males present a higher dorsal fin. These somatic changes are probably related to the swimming capacity (speed, agility, maneuvering) during the breeding season and/or foraging activities. A linear model of growth was used to determine possible proportional changes with respect to total body length through the development of 33 external characteristics. The anterior region of the body and the flippers were relatively larger in immature individuals than in mature ones.

Week of 20 January 2014

INES CARVALHO, JACQUELINE AY-LING LOO, TIM COLLINS, J. BARENDSE, CRISTINA POMILLA, **MATTHEW S. LESLIE**, PETER BEST, HOWARD ROSENBAUM. 2014. Does temporal and spatial segregation explain the complex population structure of humpback whales on the coast of West Africa? Marine Biology http://link.springer.com/article/10.1007/s00227-013-2379-1

Abstract - Humpback whales (Megaptera novaeangliae) in the Southeastern Atlantic Ocean (BSB stock) are distributed in winter along the western coast of the African continent, from Gulf of Guinea to western South Africa. Recent data suggest that this stock is sub-structured with a sub-stock that breeds in Gabon and possibly in other areas of Gulf of Guinea through Angola (B1), and a sub-stock using the west coast of South Africa as a winter migration corridor and summer feeding ground (B2). The location of the breeding ground for B2 whales remains unknown. This work re-evaluates the spatial and temporal population structure of humpback whales on the west coast of Africa using a combination of maternally and bi-parentally inherited markers. A total of 2018 samples representing B1 and B2 regions were amplified, sexed, genotyped and sequenced. The results revealed a subtle but significant genetic differentiation at spatial and temporal scales between B1 and B2, even with high gene flow and current interchange between the two regions. Differences in site fidelity and sex ratio between the two sub-stocks were found. The existence of some spatial and/or temporal segregation for the breeding grounds in the Gulf of Guinea together with the possible maternally directed site-fidelity to specific feeding grounds, some animals from Gabon travelling offshore to feeding grounds and others travelling coastwise to feed off west South Africa could be an explanation for the nature of the genetic differentiation found in this study. Further genetic sampling in other areas of the winter range and the strategic deployment of satellite tags could help clarify the situation.

Oliveira, L. R. and **Brownell, R. L., Jr.** 2014. Taxonomic status of two subspecies of South American fur seals: *Arctocephalus australis australis* vs. *A. a. gracilis*. Marine Mammal Science DOI: 10.1111/mms.12098 *Summary* – Based on morphology, genetics, and distribution, we conclude that there are differences at the ESU, subspecies or species level between Peru (and northern Chile), and the western South Atlantic (Brazil, Uruguay, Argentina, and the Falkland Islands), and eastern South Pacific (southern Chile) fur seals. We propose that *A. a. gracilis* is a junior synonym of *A. a. australis*. The English common name should remain the South American fur seal

on the South Atlantic mainland and the Falkland Islands. Following Berta and Churchill (2012) the Peru/northern fur seal is an unnamed subspecies with the Peruvian fur seal as its English common name. However, additional studies are needed on Peruvian and Galapagos fur seals to determine their taxonomic status and relationship to other fur seals.

Week of 13 January 2014

Galletti Vernazzani, B., Cabrera, E., and **Brownell, R. L., Jr**. 2014. Eastern South Pacific southern right whale photo-identification catalog reveals behavior and habitat use patterns. Marine Mammal Science 30(1):389-398. *No Abstract*

Week of 6 January 2014

Elisabeth Slooten, John Y. Wang, Sarah Z. Dungan, **Karin A. Forney**, Samuel K. Hung, **Thomas A. Jefferson**, Kimberly N. Riehl, Lorenzo Rojas-Bracho, Peter S. Ross, Ashley Wee, Robin Winkler, Shih-Chu Yang, Chaolun A. Chen. 2013. Impacts of fisheries on the Critically Endangered humpback dolphin *Sousa chinensis* population in the eastern Taiwan Strait. Endangered Species Research Vol. 22: 99–114, doi: 10.3354/esr00518

Abstract - Biological and fisheries data were analysed to assess the impact of fisheries mortality on a Critically Endangered subpopulation of <100 humpback dolphins Sousa chinensis in the eastern Taiwan Strait (ETS). Substantial interactions between ETS S. chinensis (hereafter Sousa) and fishing gear are known to cause dolphin mortality. In 2009, a total of 6318 motorised fishing vessels were operating from ports within Sousa habitats. An average of 32 fishing craft per kilometer was observed along a 200 km stretch of Sousa habitat. Based on a photo-identification catalogue, >30% of the ETS Sousa subpopulation exhibited injuries caused by fishing gear. Three individuals were photographed with fishing gear attached to their bodies, and 1 dolphin was found dead with fresh injuries caused by fishing gear. To ensure recovery of ETS Sousa, mortality due to human causes should be reduced to <1 individual every 7 yr. Fisheries bycatch is the most serious threat to these dolphins and needs to be eliminated as soon as possible to avoid extinction. Preventing the use of trammel nets, other gillnets and trawling throughout their habitat would be the single most effective conservation measure for ETS Sousa in the short term. Other fishing methods are available, and using the most selective, sustainable fishing methods available will benefit not only dolphins but also fish stocks, seabirds and other species, as well as the fishing industry, which depends on these species for its long-term viability. However, in the short term, there are costs associated with switching to more selective fishing gear.

Week of 2 December 2013

Karen K. Martien, David P. Gregovich, André E. Punt. 2013. Defining the appropriate 'Unit-To-Conserve' under the International Whaling Commission's Revised Management Procedure. Journal of Cetacean Research and Management, **13**:31-38.

Abstract - Identifying the appropriate 'Unit to Conserve' (UTC) is critical to the success of any management scheme. While the need to define the UTC appropriate to the IWC's Catch Limit Algorithm (CLA) has long been recognised by its Scientific Committee, little progress has been made on this issue. The CLA was rigorously tested prior to its adoption. However, most of those original performance trials focused on singlepopulation scenarios or two-population scenarios with no ongoing dispersal. None of the trials considered the performance of the CLA across a range of dispersal rates. In this study, the performance of the CLA under a variety of population structure scenarios is examined. This is the first study to investigate the levels of connectivity (i.e. dispersal rate) for which populations require separate management to meet the conservation goals of the CLA. All the trials consisted of two populations that were managed as a single stock for 100 years. Both historical and modern hunts were spatially-biased so that population 1 was the primary target of hunting. Parameters that varied among trials were the relative carrying capacities (K) of the populations, the dispersal rate between them, maximum sustainable yield rate (MSYR1+), and the precision in simulated abundance estimates. All of these parameters had strong effects on the conservation performance of the CLA. Trials with a low MSYR1+ (1%) generally ended with the abundance of population 1 below 0.54K, regardless of the dispersal rate or relative carrying capacities of the two populations. The same was true of trials in which the carrying capacity of population 1 represented only 10% of the total landscape carrying

capacity and the CV of the abundance estimates was low, even when dispersal between populations was high $(5 \times 10-3\text{yr}-1)$ and MSYR1+ was 4%. The results suggest that the appropriate UTCs under the RMP are likely to exchange dispersers at high enough rates that they will be difficult to delineate using existing methods. These results also highlight the value of spatially-diffuse hunting patterns that avoid potential overhunting of unrecognised stocks.

Wallace, B.P., **Tiwari, M**. & Girondot, M. 2013. *Dermochelys coriacea*. In: IUCN 2013. IUCN Red List of Threatened Species. Version 2013.2. www.iucnredlist.org>.

Overview - This assessment is significant in that it is the first time subpopulation-level listings for Leatherback turtles are recognized by IUCN along with the global assessment of all subpopulations combined. Based on Red List criteria and categories, East Pacific, West Pacific, Southwest Atlantic, and Southwest Indian Ocean subpopulations were listed as "Critically Endangered," Northwest Atlantic leatherbacks were listed as "Least Concern," and Northeast Indian Ocean and Southeast Atlantic subpopulations were listed as "Data Deficient". Globally, leatherback status is now "Vulnerable."

Week of 25 November 2013

Hyung-Soon Yim and 54 co-authors (including **Phil Morin**). 2013. Minke whale genome and aquatic adaptation in cetaceans. Nature Genetics. doi.10.1038/ng.2835

Abstract - The shift from terrestrial to aquatic life by whales was a substantial evolutionary event. Here we report the whole-genome sequencing and *de novo* assembly of the minke whale genome, as well as the whole-genome sequences of three minke whales, a fin whale, a bottlenose dolphin and a finless porpoise. Our comparative genomic analysis identified an expansion in the whale lineage of gene families associated with stress-responsive proteins and anaerobic metabolism, whereas gene families related to body hair and sensory receptors were contracted. Our analysis also identified whale-specific mutations in genes encoding antioxidants and enzymes controlling blood pressure and salt concentration. Overall the whale-genome sequences exhibited distinct features that are associated with the physiological and morphological changes needed for life in an aquatic environment, marked by resistance to physiological stresses caused by a lack of oxygen, increased amounts of reactive oxygen species and high salt levels.

Victoria J. Rowntree, Marcela M. Uhart, Mariano Sironi, Andrea Chirife, Matias Di Martino, Luciano La Sala, Luciana Musmeci, Nadia Mohamed, Julian Andrejuk, Denise McAloose, Juan Emilio Sala, Alejandro Carribero, Heather Rally, Marcelo Franco, Frederick R. Adler, **Robert. L. Brownell Jr.,** Jon Seger, Teri Rowles. 2013. Unexplained recurring high mortality of southern right whale *Eubalaena australis* calves at Península Valdés, Argentina. Marine Ecology Progress Series 493: 275–289. doi: 10.3354/meps10506

Abstract - Hundreds of southern right whale calves *Eubalaena australis* died on their calving ground at Península Valdés, Argentina from 2003 through 2011. During this period, the number of dead calves increased at a much greater rate than that of living calves over the preceding 32 yr, and with greater interannual variation. High mortality events occurred late in the calving seasons of 2005 and 2007, early in the seasons of 2008 and 2009, and were equally divided between early and late in 2010 and 2011. Calves that died late in the seasons of 2005 and 2007 were at least a meter longer (mean 7.3 m) than newborns, indicating that they had grown and presumably were healthy before dying. An unusual number of large calves (>6 m) died early in the seasons of 2008 and 2009, suggesting that a population-wide process (e.g. nutritional stress) affected many mothers including older, larger mothers that tend to give birth to larger calves early in the season. Many tissue samples have been collected and analyzed, but no consistent lesions, pathologic processes or elevated levels of algal biotoxins have been identified to explain these recent mortality events. Here, we document the high mortality events, place them in historical context and describe ongoing efforts to identify their causes. As of 2010, the southern right whale sub-population that calves off Península Valdés was estimated to be less than 20% of its initial size before whaling; the ongoing high mortality of calves will significantly affect its recovery.

Week of 12 November 2013

Erin L LaCasella, Sheryan P Epperly, **Michael P Jensen,** Lesley Stokes, **Peter H Dutton.** Genetic stock composition of loggerhead turtles (*Caretta caretta*) bycaught in the oceanic waters of the North Atlantic. Endangered Species Research 22: 73–84.

Abstract - Sea turtle populations disperse widely across oceans and migrate between terrestrial nesting habitat and distant feeding and developmental habitats. Understanding population stock structure is important for accurately assessing threats such as mortality from fishery bycatch and for defining specific demographic units of conservation concern. We compared 776-bp mtDNA control region haplotypes from 389 juvenile loggerhead turtles sampled as bycatch in the U.S. pelagic longline fishery in the western North Atlantic Northeast Distant (NED) region to haplotype frequencies observed in 23 genetically distinct nesting stocks representing the 4 Distinct Population Segments (DPS) that have been identified throughout the Atlantic Ocean and Mediterranean Sea. We used Bayesian mixed-stock analysis to produce stock composition estimates for juvenile loggerhead turtles that use pelagic habitat in the central North Atlantic. We found that nearly all of the loggerheads caught in NED waters belonged to the Northwest Atlantic DPS (mean = 99.2%), with the majority coming from the large eastern Florida rookeries (mean = 84.0%). We also detected contributions from the western Florida rookeries (mean = 11.7%) and Mexico (mean = 3.5%) but found little evidence of contributions from the rookeries of the South Atlantic, Northeast Atlantic or Mediterranean DPSs. These results will help improve specific threats assessments and are relevant to ongoing development of conservation plans that are aligned to the recent DPS listings for loggerheads.

Holly Fearnbach • **John W. Durban** • David K. Ellifrit • Janice M. Waite • Craig O. Matkin • Chris R. Lunsford • Megan J. Peterson • **Jay Barlow** • Paul R. Wade. 2013. Spatial and social connectivity of fish-eating "Resident" killer whales (*Orcinus orca*) in the northern North Pacific. Marine Biology. DOI 10.1007/s00227-013-2351-0

Abstract - The productive North Pacific waters of the Gulf of Alaska, Aleutian Islands and Bering Sea support a high density of fish-eating "Resident" type killer whales (Orcinus orca), which overlap in distribution with commercial fisheries, producing both direct and indirect interactions. To provide a spatial context for these interactions, we analyzed a 10-year dataset of 3,058 whale photoidentifications from 331 encounters within a large (linear ~4,000 km) coastal study area to investigate the ranging and social patterns of 532 individually identifiable whales photographed in more than one encounter. Although capable of large-scale movements (maximum 1,443 km), we documented ranges generally <200 km, with high site fidelity across summer sampling intervals and also re-sightings during a winter survey. Bayesian analysis of pairwise associations identified four defined clusters, likely representing groupings of stable matrilines, with distinct ranging patterns, that combined to form a large network of associated whales that ranged across most of the study area. This provides evidence of structure within the Alaska stock of Resident killer whales, important for evaluating ecosystem and fisheries impacts. This network included whales known to depredate groundfish from longline fisheries, and we suggest that such large-scale connectivity has facilitated the spread of depredation.

Punt, A. E., and **J. E. Moore**. 2013. Seasonal gray whales in the Pacific Northwest: An assessment of optimum sustainable population level for the Pacific Coast Feeding Group. NOAA Technical Memorandum NMFS-SWFSC-518.

Week of 04 November 2013

Michael P Jensen, Colin J. Limpus, Scott D. Whiting, Michael Guinea, Robert I. T. Prince, Kiki Dethmers, Ida Bagus Windia Adnyana, Rod Kennett, Nancy N. FitzSimmons. 2013. Defining olive ridley turtle (*Lepidochelys olivacea*) management units in Australia and assessing the potential impact of mortality in ghost nets. Endangered Species Research 21: 241–253.

Abstract - In Australia, the olive ridley sea turtle *Lepidochelys olivacea* has received little research attention and monitoring. The Australian populations are relatively small and their distribution is limited to remote

areas in the northern part of the country. Previous global genetic studies of olive ridley populations showed that the Australian breeding population at the McCluer Group of islands, Northern Territory, is genetically distinct from other olive ridley populations breeding in the Indo-Pacific. However, nothing is known about the genetic stock structure among Australian olive ridley rookeries found across northern Australia. High predation of eggs by feral pigs, dogs and monitor lizards *Varanus* spp. is believed to have severely impacted the number of nesting females at some rookeries. Of particular concern is the small nesting population on the western Cape York Peninsula, and without immediate conservation action this population could face extinction. The results presented here establish that there are at least 2 independent management units (stocks) of olive ridley turtles nesting in Australia and emphasise the importance of conserving the genetically distinct small breeding population nesting along the western Cape York Peninsula. In addition, results from 44 turtles caught in ghost nets across the Gulf of Carpentaria revealed that 45% of the haplotypes (32% of all ghost net samples) had not been observed at any rookery in Australia or SE Asia. This research highlights the need for better information on olive ridley population structure in the region and for urgent conservation action for the western Cape York population.

Jones TT, Van Houtan KS, Bostrom BL, Ostafichuk P, Mikkelsen J, Tezcan E, Carey M, Imlach B, **Seminoff JA** (2013) Calculating the ecological impacts of animal-borne instruments on aquatic organisms. Methods in Ecology and Evolution doi:10.1111/2041-210X.12109

Summary:

1. Animal-borne instruments provide researchers with valuable data to address important questions on wildlife ecology and conservation. However, these devices have known impacts on animal behaviour and energetics. Tags deployed on migrating animals may reduce reproductive output through increased energy demands or cause phenological mismatches of foraging and nesting events. For marine organisms, the only tagging guidelines that exist are based on lift and thrust impacts on birds – concepts that do not translate well to aquatic animals. Herein, we provide guidelines on assessing drag from animal-borne instruments and discuss the ecological impacts on marine organisms. Of particular concern is the effect of drag from instruments to the welfare of the animals and for the applicability of collected data to wild populations. 2. To help understand how drag from electronic tags affects marine animals in the wild, we used marine turtles as model aquatic organisms and conducted wind tunnel experiments to measure the fluid drag of various marine turtle body types with and without commercially available electronic tags (e.g. satellite, TDR, video cameras). We quantified the drag associated with carrying biotelemetry devices of varying frontal area and design (squared or tear drop shaped) and generated contour plots depicting percentage drag increase as a framework for evaluating tag drag by scientists and wildlife managers. Then, using concepts of fluid dynamics, we derived a universal equation estimating drag impacts from instruments across marine taxa. 3. The drag of the marine turtle casts was measured in wind speeds from 2 to 30 m/s, equivalent to 01-19 m/s in seawater. The drag coefficient (CD) of the marine turtles ranged from 011 to 022, which is typical of other large, air-breathing, marine vertebrates. The CD of tags in reference to the turtle casts was 091'018 and most tags caused minimal additional drag (<5%) to adult animals, but the same devices increased the drag for juveniles significantly (>100%). The sensitivity of aquatic animals to instrument drag is a dynamic relationship between the fluid flow patterns, or CD, and the frontal area ratio of the animal and tag. 4. In this paper, we have outlined methods for quantifying the drag costs from animal-borne instrumentation considering the instrument retention time (time to release from the animal) and the activity of the instrumented animal. With this valuable tool, researchers can quantify the drag costs from animal-borne instrumentation and choose appropriate tags for their intended study organism and question. Reducing drag will ultimately reduce the impact on the instrumented animals and lead to greater biological realism in the collected data.

Sara M. Maxwell, Elliott L. Hazen, Steven J. Bograd, Benjamin S. Halpern, Greg A. Breed, Barry Nickel, Nicole M. Teutschel, Larry B. Crowder, **Scott Benson, Peter H. Dutton**, Helen Bailey, Michelle A. Kappes, Carey E. Kuhn, Michael J. Weise, Bruce Mate, Scott A. Shaffer, Jason L. Hassrick, Robert W. Henry, Ladd Irvine, Birgitte I. McDonald, Patrick W. Robinson, Barbara A. Block, & Daniel P. Costa. 2013. Cumulative human impacts on marine predators. Nature Communications DOI: 10.1038/ncomms3688.

Abstract - Stressors associated with human activities interact in complex ways to affect marine ecosystems, yet we lack spatially explicit assessments of cumulative impacts on ecologically and economically key components such as marine predators. Here we develop a metric of cumulative utilization and impact (CUI) on marine predators by combining electronic tracking data of eight protected predator species (n½685 individuals) in the California Current Ecosystem with data on 24 anthropogenic stressors. We show significant variation in CUI with some of the highest impacts within US National Marine Sanctuaries. High variation in underlying species and cumulative impact distributions means that neither alone is sufficient for effective spatial management. Instead, comprehensive management approaches accounting for both cumulative human impacts and trade-offs among multiple stressors must be applied in planning the use of marine resources.

Week of 29 October 2013

Avens L, Goshe LR, Pajuelo M, Bjorndal KA, MacDonald BD, Lemons GE, Bolten AB, **Seminoff JA** (2013) Complementary skeletochronology and stable isotope analyses offer new insight into juvenile loggerhead sea turtle oceanic stage duration and growth dynamics. Marine Ecology Progress Series 491: 235–251.

Abstract - Stage durations are integral to wildlife population models that can inform management, as they influence age at maturation and stage-specific survival rates. To refine oceanic stage duration estimates for western North Atlantic loggerhead sea turtles Caretta caretta, skeletochronological analysis was conducted on humeri collected in the Azores islands and along the US Atlantic coast. Complementary skeletal growth increment-specific stable isotope analysis was also performed for a subset of the humeri, to identify the skeletal growth mark associated with the shift from oceanic to neritic habitat through stable nitrogen isotope $(\delta 15N)$ values and the presence of turtles in inshore waters. Although the transitional growth mark in this sub-sample corresponded to a range of sizes similar to those described in previous studies, mean size at recruitment (55.3 cm straightline carapace length [SCL]) for these turtles was larger than previously estimated. Similarly, while the range of ages at recruitment — corresponding both with the transitional growth mark and those yielded by fitting smoothing splines to SCL-at-age data—overlapped almost fully with earlier estimates, the mean age estimate (12.4 yr) differed from previous studies. Validated backcalculation of somatic growth rates from skeletal growth marks yielded means and ranges that encompassed those of previous loggerhead growth studies in this geographic area. Generalized additive models and generalized additive mixed models used to assess the potential influence of discrete and continuous covariates on back-calculated growth rates spanning 1984 to 2009 indicated significant effects of age, SCL, calendar year, and $\delta 15N$, but none for sex or location.

Robin W. Baird, Erin M. Oleson, **Jay Barlow**, Allan D. Ligon, Antoinette M. Gorgone, and Sabre D. Mahaffy. Evidence of an Island-Associated Population of False Killer Whales (*Pseudorca crassidens*) in the Northwestern Hawaiian Islands. Pacific Science (2013), vol. 67, no. 4:513 – 521. doi:10.2984/67.4.2

Abstract - Two populations of false killer whales, *Pseudorca crassidens*, are recognized from Hawaiian waters: the Hawaiian insular population, an island-associated population found around the main Hawaiian Islands; and the Hawaii1 pelagic population, found in offshore waters. This species has not been previously documented near the Northwestern Hawaiian Islands. During a 2010 large-vessel survey throughout the Exclusive Economic Zone (EEZ) surrounding the Hawaiian Islands, false killer whales from 11 encounters were individually photo-identified, and photos were compared among encounters and with a catalog of false killer whales from the main Hawaiian Islands. Individuals from three of the encounters, all in the Northwestern Hawaiian Islands within the eastern part of the Papahänaumokuäkea Marine National Monument, were the only ones documented that matched with false killer whales previously seen around the main Hawaiian Islands, and the matches were to individuals documented off Kaua'i in 2008 that were of unknown population membership. Two individuals from one of these three 2010 encounters were instrumented with satellite tags attached to dorsal fins, and their movements were documented over 4.6 and 52 days. Movements of the tagged individuals ranged from French Frigate Shoals to Middle Bank (between Nihoa and Ni'ihau) and included shallow nearshore waters and deep waters to 147 km from land. Combined,

the photo-identification and satellite-tagging results suggest that there is a second island-associated population of this species in Hawai'i that primarily uses the Northwestern Hawaiian Islands, with a range that overlaps with that of the main Hawaiian Islands insular population.

Kershaw, F., Leslie, M.S., Collins, T., Mansur, R., Smith, B., Minton, G., Baldwin, R., LeDuc, R., Anderson, R.C., Brownell, R.L. Jr., Rosenbaum, H.C. 2013. Population Differentiation of Two Forms of Bryde's Whale in the Indian and Pacific Oceans. Journal of Heredity. doi:10.1093/jhered/est057

Abstract - Accurate identification of units for conservation is particularly challenging for marine species as obvious barriers to gene flow are lacking. Bryde's whales (Balaenoptera spp.) are subject to multiple human-mediated stressors, including fisheries bycatch, ship strikes and scientific whaling by Japan. For effective management, a clear understanding of how populations of each Bryde's whale species are genetically structured across their range is required. We conducted a population-level analysis of mtDNA control region sequences with 56 new samples from Oman, Maldives, and Bangladesh, plus published sequences from Java and the Northern Pacific. Nine diagnostic characters in the mitochondrial control region and a maximum parsimony phylogenetic analysis identified 2 genetically recognized subspecies of Bryde's whale: the larger, offshore form, Balaenoptera edeni brydei, and the smaller, coastal form, Balaenoptera edeni edeni. Genetic diversity and differentiation indices, combined with a reconstructed maximum parsimony haplotype network, indicate strong differences in the genetic diversity and population structure within each subspecies. Discrete population units are identified for B. e. brydei in the Maldives, Java and the Northwest Pacific and for B. e. edeni between the Northern Indian Ocean (Oman and Bangladesh) and the coastal waters of Japan.

Ng, C. K-Y., **P.H. Dutton**, S. K-F. Chan, K-S. Cheung, J-W. Qiu, and Y-N. Sun. 2013. Characterization and conservation concern of green turtles (*Chelonia mydas*) nesting in Hong Kong, China. Pacific Science 68 (2): (Early View)

Abstract - Hong Kong holds one of the last remaining nesting populations of endangered green turtles (Chelonia mydas) in southern China. Bearing in mind that nesting individuals are vital to sustain populations, this study characterizes and reports essential baseline information about the nesting pattern, post-nesting movement and genetic composition of green turtles nesting in Hong Kong in order to provide a basis for effective scientific-based management of this migratory species. While the number of nesters observed in Hong Kong was relatively low compared with other rookeries in southern China, the nesting pattern in terms of clutch size and inter-nesting interval was comparable to that of other nearby rookeries. These nesters are likely a remnant of the small population previously depleted as a result of the historical harvesting of eggs in Hong Kong. Based on the available DNA sequences and literature, we identified two mtDNA haplotypes: CmP18 which is also common in the rookery in Taiwan and a novel endemic haplotype (CmP116), and found significant differentiation based on haplotype frequencies between Hong Kong and Lanyu, Taiwan (FST=0.90, p<0.001), indicating that these nesting populations are demographically isolated. Loss of these populations would therefore result in loss of genetic diversity for this species in the region. Satellite tracking of the local nesters revealed post-nesting movement to foraging habitats in Vietnam and Hainan Island. International cooperation and consistent dedicated research are of paramount importance to the conservation and recovery of the green turtle assemblages in the region.

Parsons, K. M., J. W. Durban, A. M. Burdin, V. N. Burkanov, R. L. Pitman, J. Barlow, L. G. Barrett-Lennard, R. G. LeDuc, K. M. Robertson, C. O. Matkin, and Paul R. Wade. 2013. Geographic patterns of genetic differentiation among killer whales in the northern North Pacific. J. Heredity 104(6):737-754.

Abstract - The difficulties associated with detecting population boundaries have long constrained the conservation and management of highly mobile, wide-ranging marine species, such as killer whales (*Orcinus orca*). In this study, we use data from 26 nuclear microsatellite loci and mitochondrial DNA sequences (988 bp) to test a priori hypotheses about population subdivisions generated from a decade of killer whale surveys across the northern North Pacific. A total of 462 remote skin biopsies were collected from wild killer whales primarily between 2001 and 2010 from the northern Gulf of Alaska to the Sea of Okhotsk, representing both the piscivorous "resident" and the mammal-eating "transient" (or Bigg's) killer whales. Divergence of the 2 ecotypes was supported by both mtDNA and microsatellites. Geographic patterns of genetic differentiation

were supported by significant regions of genetic discontinuity, providing evidence of population structuring within both ecotypes and corroborating direct observations of restricted movements of individual whales. In the Aleutian Islands (Alaska), subpopulations, or groups with significantly different mtDNA and microsatellite allele frequencies, were largely delimited by major oceanographic boundaries for resident killer whales. Although Amchitka Pass represented a major subdivision for transient killer whales between the central and western Aleutian Islands, several smaller subpopulations were evident throughout the eastern Aleutians and Bering Sea. Support for seasonally sympatric transient subpopulations around Unimak Island suggests isolating mechanisms other than geographic distance within this highly mobile top predator.

Pitman, R.L. 2013. Marine Mammal Science 29(4): 777–779.

Book Review: MARINE MAMMAL SPECIES OF INDIA. E. Vivekanandan and R. Jeyabaskaran.

ISBN:978-8-923271-5-0. Central Marine Fisheries Research Institute, Kochi, India.

2012. 228 pp., 146 color illustrations, 32 tables. US\$50.00.

DOI: 10.1111/mms.12061

Rankin, S., F. Archer, and J. Barlow. 2013. Vocal activity of tropical dolphins is inhibited by the presence of killer whales, *Orcinus orca*. Marine Mammal Science 29(4):679-690.

Abstract - Research has suggested killer whale (*Orcinus orca*) predation may affect cetacean vocal behavior; however, few data exist to test this hypothesis. Data collected during 40,976 km of visual and acoustic shipboard surveys in the tropical Pacific Ocean, including 1,232 detections of 13 species, were examined to determine if changes in dolphin vocal activity could be attributed to the presence of killer whales. Generalized linear models and Random Forest analyses were used to test the hypothesis that dolphin vocal activity was related to the distance and time to the nearest killer whale sighting. Both results show that dolphin vocalizations were inversely correlated with the temporal proximity of killer whales (P < 0.05). Despite the relative rarity of killer whales in the tropics, they appear to influence vocal behavior of nearby dolphin schools. This disruption in communication may not significantly impact interactions necessary for survival in tropical waters where killer whale density is low. However, in temperate climates, where increased productivity supports a greater abundance of killer whales, this interruption in communication may have a greater impact. The lower incidence of whistling dolphins in temperate waters may be related to the greater abundance of killer whales in these areas.

Zárate P, Bjorndal KA, Parra M, **Dutton PH**, **Seminoff JA**, Bolten AB (2013) Hatching and emergence success in green turtle *Chelonia mydas* nests in the Galápagos Islands. Aquatic Biology 19: 217–229.

Abstract - The interactions of numerous abiotic and biotic factors experienced by sea turtle embryos during incubation affect their survival. In this study we determined the hatching and emergence success of green turtles Chelonia mydas from nests on 4 beaches on the Galápagos Islands, one of the most important rookeries for green turtles in the eastern Pacific Ocean. Mean (±SD) hatching and emergence success for the 1039 nests examined were 46.0 ± 33.4 and $45.6 \pm 33.4\%$, respectively. These values are relatively low compared to other green turtle populations worldwide. We evaluated the effects of beach, year, day of oviposition, carapace length and width of female, nest position, nest habitat, and nest chamber depth on hatching and emergence success with binomial generalized additive models with fixed effects. We found variation in hatching and emergence success was significant among beaches, years, day of oviposition, and nest habitat. Predation by feral pigs and beetles and destruction of earlier nests by nesting females were the most important causes of embryo mortality. Efforts to keep threats at minimum levels, particularly controlling pigs near Isabela beaches, should be considered a major conservation objective. This study highlights important differences among beaches within a rookery and emphasizes the need to continue improving management strategies to protect green turtles and their critical habitats. Quantitative information provided here can be used as a basis for long-term studies in the Galápagos and for comparison to other sea turtles rookeries.

Week of 30 September 2013

Keating, J.L. and **J. Barlow**. 2013. Summary of Pamguard beaked whale click detectors and classifiers used during the 2012 Southern California Behavioral Response Study. NOAA Technical Memorandum, NOAA-TM-NMFS-SWFSC-517. Available at http://swfsc.noaa.gov/submenu.aspx?&ParentMenuId=32

Week of 16 September 2013

Foote, A.D., **Morin, P.A., Pitman, R.L.**, Ávila-Arcos, M.C., **Durban, J.W.**, van Helden, A., Sinding, M.-H.S., Gilbert, M.T.P., 2013. Mitogenomic insights into a recently described and rarely observed killer whale morphotype. Polar Biology 36, 1519-1523.

Abstract - Identifying evolutionary divergent taxonomic units, e.g. species and subspecies, is important for conservation and evolutionary biology. The 'type D' killer whale, *Orcinus orca*, is a rarely observed morphotype with a pelagic, circumpolar subantarctic distribution, making dedicated research and therefore taxonomic study extremely difficult to date. In this study, we used DNA target enrichment hybridisation capture coupled to high throughput sequencing, to obtain the first DNA sequence from the only known museum specimen of this recently described morphotype. The high coverage, complete mitogenome sequence was compared to a previously published global dataset of 139 individuals, indicating that this type is highly divergent to all previously genetically sequenced killer whale forms. The estimated divergence time (390,000 years ago) from its most recent common ancestor with other extant killer whale lineages was the second oldest split within the killer whale phylogeny. This study provides the first genetic support of type D potentially being a distinct subspecies or species of killer whale, although further samples are needed to identify whether there is monophyly of mitogenome sequences and whether nuclear DNA also indicates reproductive isolation. These findings also highlight the value of natural history museum collections and new technologies to investigate the taxonomy of rare, cryptic or difficult to access species.

Week of 9 September 2013

Barlow, J., P. L. Tyack, M. P. Johnson, R. W. Baird, G. S. Schorr, R. D. Andrews, and N. Aguilar de Soto. 2013. Trackline and point detection probabilities for acoustic surveys of Cuvier's and Blainsville's beaked whales. J. Acoust. Soc. Am. 134(3): 2486-2496.

Abstract - Acoustic survey methods can be used to estimate density and abundance using sounds produced by cetaceans and detected using hydrophones if the probability of detection can be estimated. For passive acoustic surveys, probability of detection at zero horizontal distance from a sensor, commonly called g(0), depends on the temporal patterns of vocalizations. Methods to estimate g(0) are developed based on the assumption that a beaked whale will be detected if it is producing regular echolocation clicks directly under or above a hydrophone. Data from acoustic recording tags placed on two species of beaked whales (Cuvier's beaked whale—Ziphius cavirostris and Blainville's beaked whale—Mesoplodon densirostris) are used to directly estimate the percentage of time they produce echolocation clicks. A model of vocal behavior for these species as a function of their diving behavior is applied to other types of dive data (from time-depth recorders and time-depth-transmitting satellite tags) to indirectly determine g(0) in other locations for low ambient noise conditions. Estimates of g(0) for a single instant in time are 0.28 (s.d. = 0.05) for Cuvier's beaked whale and 0.19 (s.d. = 0.01) for Blainville's beaked whale.

Tina M. Yack, Jay Barlow, John Calambokidis, Brandon Southall, and Shannon Coates. 2013. Identification of previously unknown beaked whale habitat in the Southern California Bight using a towed hydrophone array. The Journal of the Acoustical Society of America 134(3): 2589–2595 [doi.org/10.1121/1.4816585]

Abstract - Beaked whales are diverse and species rich taxa. They spend the vast majority of their time submerged, regularly diving to depths of hundreds to thousands of meters, typically occur in small groups,

and behave inconspicuously at the surface. These factors make them extremely difficult to detect using standard visual survey methods. However, recent advancements in acoustic detection capabilities have made passive acoustic monitoring (PAM) a viable alternative. Beaked whales can be discriminated from other odontocetes by the unique characteristics of their echolocation clicks. In 2009 and 2010, PAM methods using towed hydrophone arrays were tested. These methods proved highly effective for real-time detection of beaked whales in the Southern California Bight (SCB) and were subsequently implemented in 2011 to successfully detect and track beaked whales during the ongoing Southern California Behavioral Response Study. The three year field effort has resulted in (1) the successful classification and tracking of Cuvier's (*Ziphius cavirostris*), Baird's (*Berardius bairdii*), and unidentified Mesoplodon beaked whale species and (2) the identification of areas of previously unknown beaked whale habitat use. Identification of habitat use areas will contribute to a better understanding of the complex relationship between beaked whale distribution, occurrence, and preferred habitat characteristics on a relatively small spatial scale. These findings will also provide information that can be used to promote more effective management and conservation of beaked whales in the SCB, a heavily used Naval operation and training region.

Week of 2 September 2013

Edwards EF, Kellar NM, and Perrin WF. 2013. Form, function and pathology in the pantropical spotted dolphin (*Stenella attenuata*). NOAA Technical Memorandum NOAA-TMNMFS-SWFSC-516. 76pp.

Summary - This report reviews, integrates and summarizes published literature regarding form, function and pathology in the pantropical spotted dolphin. Because the pantropical spotted dolphin is one of the primary species targeted by the tuna purse-seine fishery in the eastern tropical Pacific Ocean (ETP), the report includes discussion of spotted dolphin morphological and physiological characteristics that may be negatively affected by interaction with the ETP purse-seine fishery.

Week of 12 August 2013

Okuyama J, Nakajima K, Noda T, Kimura S, Kamihata H, et al. 2013. Ethogram of Immature Green Turtles: Behavioral Strategies for Somatic Growth in Large Marine Herbivores. PLoS ONE 8(6): e65783. doi:10.1371/journal.pone.0065783.

Abstract - Animals are assumed to obtain/conserve energy effectively to maximise their fitness, which manifests itself in a variety of behavioral strategies. For marine animals, however, these behavioral strategies are generally unknown due to the lack of high-resolution monitoring techniques in marine habitats. As large marine herbivores, immature green turtles do not need to allocate energy to reproduction but are at risk of shark predation, although it is a rare occurrence. They are therefore assumed to select/use feeding and resting sites that maximise their fitness in terms of somatic growth, while avoiding predation. We investigated fine-scale behavioral patterns (feeding, resting and other behaviors), microhabitat use and time spent on each behavior for eight immature green turtles using data loggers including: depth, global positioning system, head acceleration, speed and video sensors. Immature green turtles at Iriomote Island, Japan, spent an average of 4.8 h feeding on seagrass each day, with two peaks, between 5:00 and 9:00, and between 17:00 and 20:00. This feeding pattern appeared to be restricted by gut capacity, and thus maximised energy acquisition. Meanwhile, most of the remaining time was spent resting at locations close to feeding grounds, which allowed turtles to conserve energy spent travelling and reduced the duration of periods exposed to predation. These behavioral patterns and time allocations allow immature green turtles to effectively obtain/conserve energy for growth, thus maximising their fitness.

Trego ML, Kellar NM, Danil K. 2013. Validation of Blubber Progesterone Concentrations for Pregnancy Determination in Three Dolphin Species and a Porpoise. PLoS ONE 8(7): e69709. doi:10.1371/journal.pone.0069709

Abstract - Recent studies have validated the use of biopsies as a minimally invasive way to identify pregnant females in several species of wild cetaceans: Balaenaptera acutorostrata, Delphinus delphis, Lissodelphis borealis, and Lagenorhynchus obliquidens. These studies found that progesterone (P4) concentrations quantified from blubber attached to biopsy samples is diagnostic of pregnancy. Here we examine a broader group of cetacean species in efforts to investigate how progesterone levels vary between species with respect to pregnancy status. We compared P4 concentrations in blubber collected from fishery bycatch and beachstranded specimens for 40 females of known reproductive condition from *Delphinus capensis* (n = 18), Stenella attenuata (n = 8), S. longirostris (n = 6), and Phocoenoides dalli (n = 8). The P4 concentrations were different (t = -7.1, p = 1.79E-08) between pregnant and nonpregnant animals in all species, with the mean blubber P4 concentration for pregnant animals 164 times higher than that of non-pregnant animals. There was no overlap in concentration levels between sexually immature or nonpregnant sexually mature animals and pregnant animals. No significant differences (F = 0.354, p = 0.559) were found between mature non-pregnant and immature D. capensis and P dalli, suggesting P4 level is not indicative of maturity state in female delphinoids. P4 concentrations in relation to reproductive state were remarkably similar across species. All samples were analyzed with two different enzyme immunoassay kits to gauge assay sensitivity to measure progesterone in small samples, such as biopsies. With the technique now validated for these cetacean species, blubber P4 is a reliable diagnostic of pregnancies across multiple species, and thus expands the utility of this method to study reproduction in free-ranging cetaceans using biopsies.

Week of 5 August 2013

T.J. Guy, S.L. Jennings, R.M. Suryan, E.F. Melvin, M.A. Bellman, **L.T. Ballance**, B.A. Blackie, D.A. Croll, T. Deguchi, T.O. Geernaert, R.W. Henry, M. Hester, K.D. Hyrenbach, J. Jahncke, M.A. Kappes, K. Ozaki, J. Roletto, F. Sato, W.J. Sydeman, J.E. Zamon. 2013. Overlap of North Pacific albatrosses with the U.S. west coast groundfish and shrimp fisheries. Fisheries Research 147:222-234.

Abstract - We used a combination of seabird data (both fishery-dependent and fishery-independent) and fishing-effort data to evaluate the relative fisheries risk of five west coast groundfish fisheries and one shrimp fishery to black-footed (*Phoebastria nigripes*), short-tailed (*P. albatrus*) and Laysan albatrosses(*P. immutabilis*). To assess risk, an overlap index was derived as the product of total fishing effort and at-sea survey density of black-footed albatross. This index was used as the primary tool to estimate overlap with the endangered, relatively rare short-tailed albatross, which show similar habitat utilization from satellite telemetry tracks. Telemetry data indicate Laysan albatross primarily occur offshore beyond observed fishing effort. Black-footed and short-tailed albatross-fishery overlap was highest at the shelf-break (201–1000 m) north of 36°N. Overlap and reported albatross mortality indicate that the sablefish (*Anoplopoma fimbria*) longline and Pacific hake (*Merluccius productus*) catcher-processor fisheries pose the greatest risk to these species; the near-shore rockfish (*Seabastes* spp.) longline, pink shrimp (*Pandalus jordani*) trawl, California halibut (*Paralichthys californicus*) trawl, and non-hake groundfish trawl fisheries pose relatively little risk. Implementing proven seabird bycatch-reduction measures will likely minimize albatross mortality in the highest-risk fishery, sablefish longline.

Week of 29 July 2013

Edward D. Weber and **Thomas J. Moore.** *Published Online.* Corrected conversion algorithms for the CalCOFI station grid and their implementation in several computer languages. CalCOFI Reports.

Abstract - Converting between geographic coordinates in latitude and longitude and the line and station sampling pattern of the California Cooperative Fisheries Investigations (CalCOFI) program is a commonly required task for conducting research on the California Current ecosystem. This note presents several corrections and clarifications to the previously published algorithms for performing these conversions. We include computer code to implement the algorithms in JavaTM, Perl, Python, and R. We note that freely available code to conduct the conversions in Fortran, Matlab®, JavaScriptTM, and Visual Basic® has

previously been published, and an online conversion tool is also available. A future version of the PROJ.4 cartographic projections library will also include support for CalCOFI conversions, thereby allowing for convenient conversions using the GRASS GIS, PostGIS, Python, Perl, R, and many other programs and programming languages.

Week of 15 July 2013

J. E. Van Noord, E. A. Lewallen and **R. L. Pitman**. 2013. Flyingfish feeding ecology in the eastern Pacific: prey partitioning within a speciose epipelagic community. Journal of Fish Biology. *doi:10.1111/jfb.12173*

Abstract – To test the hypothesis that prey partitioning contributes to community stability in flyingfish, the gut contents of 359 flyingfish specimens (representing five genera and eight species within Exocoetidae and Hemiramphidae) were collected at 50 dip-net stations during hour-long night-time fishing in oceanic waters of the eastern tropical Pacific Ocean between August and November 2007. Analyses using multidimensional scaling, and analysis of similarity revealed significant dietary differences among species, and similarity percentages tests helped identify the specific prey taxa responsible for these differences. Six species specialized on copepods (58 • 3–96 • 9% by number), but targeted different families. Specifically, the barbel flyingfish Exocoetus monocirrhus (n = 205) focused on euchaetids ($51 \cdot 6\%$), the banded flyingfish Hirundichthys marginatus (n = 24) fed on pontellids (21 · 8%), while the tropical two-wing flyingfish Exocoetus volitans (n = 11) and the bigwing halfbeak Oxyporhamphus micropterus (n = 34) ingested calanoids (54 \cdot 6 and 17 \cdot 0%). In contrast, the whitetip flyingfish Cheilopogon xenopterus (n = 73) and the mirrorwing flyingfish Hirundichthys speculiger (n = 4) had generalized diets comprising similar proportions of amphipod, copepod, mollusc and larval fish prey. Distinct differences in mean fullness, highly digested material, per cent empty guts and mean numbers of prey per gut were also synthesized, and uncovered a pattern of asynchronous feeding. Altogether, these findings provide valuable descriptive data on the diets of an understudied group of epipelagic teleosts, and, by extension, suggest that prey partitioning (taxa and feeding times) may influence flyingfish feeding ecology by reducing interspecific competition.

Kim M. Parsons, **John W. Durban**, Alexander M. Burdin, Vladimir N. Burkanov, **Robert L. Pitman, Jay Barlow**, Lance G. Barrett-Lennard, Richard G. LeDuc, **Kelly M. Robertson**, Craig O. Matkin, and Paul R. Wade. 2013. Geographic Patterns of Genetic Differentiation among Killer Whales in the Northern North Pacific. Journal of Heredity. *doi:10.1093/jhered/est037*

Abstract - The difficulties associated with detecting population boundaries have long constrained the conservation and management of highly mobile, wide-ranging marine species, such as killer whales (Orcinus orca). In this study, we use data from 26 nuclear microsatellite loci and mitochondrial DNA sequences (988 bp) to test a priori hypotheses about population subdivisions generated from a decade of killer whale surveys across the northern North Pacific. A total of 462 remote skin biopsies were collected from wild killer whales primarily between 2001 and 2010 from the northern Gulf of Alaska to the Sea of Okhotsk, representing both the piscivorous "resident" and the mammal-eating "transient" (or Bigg's) killer whales. Divergence of the 2 ecotypes was supported by both mtDNA and microsatellites. Geographic patterns of genetic differentiation were supported by significant regions of genetic discontinuity, providing evidence of population structuring within both ecotypes and corroborating direct observations of restricted movements of individual whales. In the Aleutian Islands (Alaska), subpopulations, or groups with significantly different mtDNA and microsatellite allele frequencies, were largely delimited by major oceanographic boundaries for resident killer whales. Although Amchitka Pass represented a major subdivision for transient killer whales between the central and western Aleutian Islands, several smaller subpopulations were evident throughout the eastern Aleutians and Bering Sea. Support for seasonally sympatric transient subpopulations around Unimak Island suggests isolating mechanisms other than geographic distance within this highly mobile top predator.

Carretta, J. V., S. M. Wilkin, M. M. Muto, and K. Wilkinson. 2013. Sources of human-related injury and mortality for U.S. Pacific west coast marine mammal stock assessments, 2007-2011. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-514, 83 p.

Abstract – The Marine Mammal Protection Act (MMPA) requires the National Oceanic and Atmospheric

Administration (NOAA), National Marine Fisheries Service (NMFS), to document human-caused mortality, non-serious injury (NSI), and serious injury (SI) of marine mammals as part of assessing marine mammal stocks and to evaluate human-caused injury and mortality levels in the context of potential biological removal (PBR) levels calculated under the MMPA (Wade 1998). NMFS defines SI as "any injury that will likely result in mortality." While recognizing mortality is straightforward, distinguishing NSI from SI requires reliable data on injury severity and animal condition, often in challenging environments where thorough examination of injuries is not possible. NMFS updated its SI designation and reporting process, which uses guidance from previous SI workshops (Angliss and DeMaster 1998, Andersen *et al.* 2008), expert opinion, and analysis of historic injury cases to develop new criteria for distinguishing SI from NSI (NOAA 2012, Moore *et al.* 2013).

This report contains records of human-caused injury and mortality to pinnipeds and cetaceans from 2007 to 2011, for marine mammal populations that occur in U.S. west coast waters and which are evaluated in Pacific region marine mammal stock assessment reports (SARs) (Carretta *et al.* 2013). Mortality records, while included, were obviously not evaluated for SI/NSI status. Subsistence and directed takes are not reported here but are reported in SARs published by NMFS.

Sources of injury data include strandings, disentanglement networks, and fishery observer programs. Stranding network data includes records of injured marine mammals at sea and ashore reported by the public, as well as researchers working in these same areas. Injury sources include, but are not limited to, *vessel strikes*, *gillnet entanglement*, *pot and trap gear entanglement*, *shootings*, *marine debris entanglement*, *research-related injuries/deaths*, *hook and line fishery interactions*, and *power plant water intake entrainment*. This report covers the 5-year period of 2007 to 2011, which includes injury and mortality data used in preparation of draft 2013 Pacific marine mammal stock assessments. Most records originate from stranding networks in California, Oregon, and Washington, though a few Alaska records of Eastern North Pacific gray whales (*Eschrichtius robustus*) are included, because this population is assessed in the Pacific region SARs and occurs along the U.S. west coast. Other marine mammals such as Steller sea lions (*Eumetopias jubatus*) occur in California, Oregon, and Washington waters, but they are assessed in Alaska region SARs and not included in this report (Allen and Angliss 2013). Injury determinations for Pacific region species/stocks in the central Pacific from Hawaii westward are also included in separate reports.

Week of 8 July 2013

Shannon Rankin, **Jay Barlow**, Yvonne Barkley, and Robert Valtierra. 2013. A guide to constructing hydrophone arrays for passive acoustic data collection during NMFS shipboard cetacean surveys. NOAA Technical Memorandum, NOAA-TM-NMFS-SWFSC-511.

Overview - This report provides a step-by-step guide to constructing a modular oil-filled towed hydrophone array to be used for passive acoustic monitoring of cetaceans from ships. This report was based on a workshop hosted by SWFSC to teach acousticians from the other NMFS science centers how to construct this hardware (funding provided by NOAA's Advanced Sampling Technologies Working Group).

Jefferson, T.A., C.R. Weir, R.C. Anderson, **L.T. Ballance**, R.D. Kenney, and J.J. Kiszka. 2013. Global patterns of Risso's dolphin (Grampus griseus) distribution: a review and critical evaluation. Mammal Review. doi:10.1111/mam.12008

Abstract - 1. The global range of Risso's dolphin *Grampus griseus* is not well known, and there has been confusion in the literature as to whether the species has a broad, circumglobal range or only occurs along continental margins.

- 2. To clarify the species' distribution and habitat preferences, we compiled and reviewed all available (published and unpublished) records of sightings and captures of this species for the past 62 years (1950–2012, n = 8068 records). Stranding records were not included.
- 3. The results showed that the species has a range that extends across ocean basins and spans between at least

64°N and 46°S, and is apparently absent from high latitude polar waters. Although Risso's dolphins occur in all habitats from coastal to oceanic, they show a strong range-wide preference for mid-temperate waters of the continental shelf and slope between 30° and 45° latitude.

4. Although a number of misconceptions about the distributional ecology of Risso's dolphin have existed, this analysis showed that it is a widespread species. It strongly favours temperate waters and prefers continental shelf and slope waters to oceanic depths. These habitat preferences appear to hold throughout much or all of the species' range.

Week of 1July 2013

Davison, P. C., D. M. Checkley Jr., J. A. Koslow, and **J. Barlow**. 2013. Carbon export mediated by mesopelagic fishes in the northeast Pacific Ocean. Progress in Oceanography

Abstract - The role of fishes in the global carbon cycle is poorly known and often neglected. We show that the biomass of mesopelagic fishes off the continental USA west to longitude 141°W is positively related to annual net primary productivity, and averages 17 g m-2. We estimate the export of carbon out of the epipelagic ocean mediated by mesopelagic fishes ("fish-mediated export"; FME) with individual-based metabolic modeling using the catch from 77 mesopelagic trawls distributed over the study area. FME was 15–17% (22–24 mg C m-2 d-1) of the total carbon exported in the study area (144 mg C m-2 d-1), as estimated from satellite data. FME varies spatially in both magnitude and relative importance. Although the magnitude of FME increases with increasing total export, the ratio of FME to total export decreases. FME exceeds 40% of the total carbon export in the oligotrophic North Pacific Subtropical Gyre, but forms <10% of the total export in the most productive waters of the California Current. Because the daytime residence depth of these fishes is below the depths where most remineralization of sinking particles occurs, FME is approximately equal to the passive transport at a depth of 400 m. The active transport of carbon by mesopelagic fishes and zooplankton is similar in magnitude to the gap between estimates of carbon export obtained with sediment traps and by other methods. FME should be considered in models of the global carbon cycle.

Week of 24 June 2013

Andrew D. Foote, **Phillip A. Morin, Robert L. Pitman**, Marı´a C. A´ vila-Arcos, **John W. Durban**, Anton van Helden, Mikkel-Holger S. Sinding, M. Thomas P. Gilbert. 2013. Mitogenomic insights into a recently described and rarely observed killer whale morphotype. Polar Biology DOI 10.1007/s00300-013-1354-0

Abstract - Identifying evolutionary divergent taxonomic units, e.g. species and subspecies, is important for conservation and evolutionary biology. The 'type D' killer whale, *Orcinus orca*, is a rarely observed morphotype with a pelagic, circumpolar subantarctic distribution, making dedicated research and therefore taxonomic study extremely difficult to date. In this study, we used DNA target enrichment hybridisation capture coupled to high throughput sequencing, to obtain the first DNA sequence from the only known museum specimen of this recently described morphotype. The high coverage, complete mitogenome sequence was compared to a previously published global dataset of 139 individuals, indicating that this type is highly divergent to all previously genetically sequenced killer whale forms. The estimated divergence time (390,000 years ago) from its most recent common ancestor with other extant killer whale lineages was the second oldest split within the killer whale phylogeny. This study provides the first genetic support of type D potentially being a distinct subspecies or species of killer whale, although further samples are needed to identify whether there is monophyly of mitogenome sequences and whether nuclear DNA also indicates reproductive isolation. These findings also highlight the value of natural history museum collections and new technologies to investigate the taxonomy of rare, cryptic or difficult to access species.

Van Noord, J. E., R. J. Olson, **J. V. Redfern**, and R. S. Kaufmann. 2013. Diet and prey selectivity in three surface-migrating myctophids in the eastern tropical Pacific. Ichthyological Research:1-4.

http://link.springer.com/article/10.1007/s10228-013-0350-2

Abstract - To test feeding selectivity, the diets of three surface-migrating myctophids [Myctophum nitidulum (n=299), Symbolophorus reversus (n=199), and Gonichthys tenuiculus (n=82)] were compared to zooplankton prey collections at 32 stations in the eastern Pacific Ocean, August-November 2006. Myctophum nitidulum fed predominately on copepods (42.7 % by number) and ostracods (41.5 %), selected amphipods (p=0.002) and ostracods (p=0.014), and avoided copepods (p<0.001). Symbolophorus reversus fed on copepods (32.5 % by number) and euphausiids (29.6 %) and selected euphausiids (p=0.002) and amphipods (p=0.008). Gonichthys tenuiculus fed on ostracods (34.6 %) and amphipods (27.3 %), but showed no significant selectivity.

Week of 17 June 2013

Paul C. Fiedler, Jessica V. Redfern, Joel Van Noord, Candice Hall, **Robert L. Pitman, Lisa T. Ballance.** 2013. Effects of a tropical cyclone on a pelagic ecosystem from the physical environment to top predators. Marine Ecology Progress Series 484:1-16.

Abstract - Tropical cyclones are environmental disturbances that may have important effects on open-ocean ecosystem structure and function, but their overall impact has rarely been assessed. The Stenella Abundance Research Line Transect and Ecosystem (STARLITE) survey, in August-November 2007, investigated spatial and temporal ecosystem variability in the eastern tropical Pacific Ocean off southwestern Mexico. Oceanographic, plankton, flyingfish, seabird, and cetacean sampling was conducted along eight 170 km transect lines, each of which were surveyed on 2 consecutive days at ~3 wk intervals. Tropical storm Kiko passed though the study area on 15-17 October and forced changes in the physical environment and in the ecosystem, from plankton to top predators. Kiko mixed water from beneath the strong, shallow thermocline to the surface. As a result, surface temperature decreased by 0.6°C, the thermocline and chlorophyll maximum layer shoaled by 10-20 m, stratification decreased by 27%, and chlorophyll increased by 33% at the surface and 35% over the euphotic zone. These changes persisted for at least 4 wk. Zooplankton biomass increased by 59% about 3 wk after the phyto -plankton increase. Changes in the stomach fullness and diet composition of planktivorous flyingfish were consistent with the increase in zooplankton biomass. Among top predators, the sighting rate of dolphins declined, while the response of seabirds varied by species and was confounded by seasonal migration patterns. Tropical cyclones are a recurrent disturbance in this region. They initiate a bottom-up forcing of the ecosystem, creating persistent patches of higher primary and secondary production, and may be regarded as a disturbance regime.

Available at http://www.int-res.com/articles/feature/m484p001.pdf

Week of 10 June 2013

Simone Baumann-Pickering, **Tina M. Yack, Jay Barlow**, Sean M. Wiggins and John A. Hildebrand. 2013. Baird's beaked whale echolocation signals. J. Acoust. Soc. Am. 133 (6).

Abstract - Echolocation signals from Baird's beaked whales were recorded during visual and acoustic shipboard surveys of cetaceans in the California Current ecosystem and with autonomous, long-term recorders in the Southern California Bight. The preliminary measurement of the visually validated Baird's beaked whale echolocation signals from towed array data were used as a basis for identifying Baird's signals in the autonomous recorder data. Two distinct signal types were found, one being a beaked whale-like frequency modulated (FM) pulse, the other being a dolphin-like broadband click. The median FM inter-pulse interval was 230 ms. Both signal types showed a consistent multi-peak structure in their spectra with peaks at 9, 16, 25, and 40 kHz. Depending on signal type, as well as recording aspect and distance to the hydrophone, these peaks varied in relative amplitude. The description of Baird's echolocation signals will allow for studies of their distribution and abundance using towed array data without associated visual sightings and from autonomous seafloor hydrophones.

Fritz L, Sweeney K, Johnson D, **Lynn M**, Gelatt T, and **Gilpatrick J.** 2013. Aerial and ship-based surveys of Steller Sea Lions (*Eumetopias jubatus*) conducted in Alaska in June-July 2008 through 2012, and an update on the status and trend of the western Distinct Population Segment in Alaska. NOAA Tech. Memo. NMFS-AFSC-251

Abstract - There is strong evidence that both the western and eastern distinct population segments (DPSs) of Steller sea lion (Eumetopias jubatus) increased in overall abundance in Alaska between 2000 and 2012. Counts of both non-pups (adults and juveniles) and pups during the breeding season in the western DPS were lowest in 2000, and increased at average rates of 1.67% per year (95% credible interval of 1.01-2.38% per year) and 1.45% per year (0.69-2.22% per year), respectively through 2012. However, there was considerable regional variability in non-pup and pup trends in 2000-2012 across the western DPS, with strong evidence of increases in three of the four regions east of Samalga Pass (eastern and western Gulf of Alaska, and eastern Aleutian Islands; ranges of 2.39% per year to 4.51% per year for non-pups and 3.03% per year to 3.97% per year for pups) being offset somewhat by both weak and strong declines in the two regions west of Samalga Pass (central and western Aleutian Islands; slow, uncertain declines in the central [-0.56% per year and -0.46% per year for non-pups and pups, respectively] and steep, certain declines in the western Aleutians [-7.23% per year and -9.36% per year for non-pups and pups, respectively]). Within the central Aleutian Islands, non-pup and pup trends varied east and west of 177°W (roughly Tanaga Pass): in the two rookery cluster areas to the east, trends were generally positive (0.51% per year and 2.25% per year for non-pups, and 2.56% per year and 0.45% per year for pups), while to the west, there was strong evidence of decline (-4.48% per year and -3.24% per year for non-pups, and -4.83% per year and -1.74% per year for pups). In southeast Alaska (eastern DPS of Steller sea lion), both non-pup and pup counts increased between 2000 and 2010, continuing the upward trend begun in the mid-1970s.

Movement of young Steller sea lions into and out of the eastern Gulf of Alaska was observed during surveys conducted 'early' and 'late' in 2008, 2009 and 2010. Analysis of the movement of sea lions branded as pups in 2000-2011 on rookeries extending from southeast Alaska through the Kodiak archipelago (including work by Jemison et al. in review) suggests a net movement from the central to the eastern Gulf of Alaska of ~1,600 sea lions during the breeding season, as well as a smaller net movement (of ~180 sea lions) from southeast Alaska to the western DPS. Inter-regional movement of this magnitude within the western DPS could affect regional trend estimation, and therefore it may be inappropriate to treat the eastern and central Gulf of Alaska as 'closed' populations; non-pup counts in the combined eastern-central Gulf of Alaska increased at 2.40% per year between 2000 and 2012. Average annual inter-DPS movement represents < 0.5% of the total number of sea lions counted in the western DPS and < 1% of those counted in southeast Alaska, and likely had a negligible impact on overall trend estimates in either area.

If the overall western non-pup count in Alaska continues to increase through 2015, the western DPS appears to be on a trajectory to satisfy the first demographic criterion for down-listing from 'endangered' to 'threatened' status under the Endangered Species Act (NMFS 2008). The second demographic criterion, however, involves regional population performance, which has varied across the range. The western DPS may satisfy the first part of criterion #2 if non-pup counts in the eastern, central and western Gulf of Alaska, eastern Aleutian Islands, and Russia (overall) continue to increase through 2015. However, persistent declines in the western Aleutian Islands and the western half of the central Aleutian Islands may preclude it from satisfying the second part of criterion #2, and indicate that the western DPS is responding to meso-scale variability in factors affecting recovery.

Week of 3 June 2013

Roden SE, Morin PA, Frey A, Balazs GH, Zarate P, Cheng I-J, Dutton PH. 2013.

Green turtle population structure in the Pacific: new insights from SNPs and microsatellites. Endangered Species Research 20: 227–234, doi: 10.3354/esr00500

Abstract: A set of nuclear single nucleotide polymorphisms (SNPs) and microsatellite markers was used to detect genetic stock structure among 5 Pacific green turtle *Chelonia mydas* nesting populations. We sampled populations in the Galapagos Islands, Ecuador (n = 57), Colola, Mexico (n = 75), French Frigate Shoals, Hawaii (n = 141), Yap, Micronesia (n = 73), and Wan-an, Taiwan (n = 57), to represent eastern, central, and western Pacific regions. A combination of 29 single independent SNPs and linked SNPs combined as

haplotypes were used for a total of 20 independent markers. In addition, 8 polymorphic microsatellite markers were applied to the same sample set. Both sets of nuclear markers confirmed significant differentiation between all sampled populations in the 3 Pacific regions ($p \le 0.001$). The use of these SNPs and microsatellites resulted in sufficient power to detect small population differences not seen in previous studies using smaller numbers of nuclear markers. Our results suggest that male-mediated gene flow between regional nesting stocks is more limited than previously believed, allowing the potential to delineate stocks more clearly. Finally, we discuss the value of SNP markers as an alternative or complement to other nuclear markers such as microsatellites for the examination of stock structure.

Week of 20 May 2013

Archer FI, Morin PA, Hancock-Hanser BL, Robertson KM, Leslie MS, et al. 2013. Mitogenomic Phylogenetics of Fin Whales (*Balaenoptera physalus spp.*): Genetic Evidence for Revision of Subspecies. PLoS ONE 8(5): e63396. doi:10.1371/journal.pone.0063396

Abstract - There are three described subspecies of fin whales (Balaenoptera physalus): B. p. physalus Linnaeus, 1758 in the Northern Hemisphere, B. p. quoyi Fischer, 1829 in the Southern Hemisphere, and a recently described pygmy form, B. p. patachonica Burmeister, 1865. The discrete distribution in the North Pacific and North Atlantic raises the question of whether a single Northern Hemisphere subspecies is valid. We assess phylogenetic patterns using ~16 K base pairs of the complete mitogenome for 154 fin whales from the North Pacific, North Atlantic - including the Mediterranean Sea - and Southern Hemisphere. A Bayesian tree of the resulting 136 haplotypes revealed several well-supported clades representing each ocean basin, with no haplotypes shared among ocean basins. The North Atlantic haplotypes (n = 12) form a sister clade to those from the Southern Hemisphere (n = 42). The estimated time to most recent common ancestor (TMRCA) for this Atlantic/Southern Hemisphere clade and 81 of the 97 samples from the North Pacific was approximately 2 Ma. 14 of the remaining North Pacific samples formed a well-supported clade within the Southern Hemisphere. The TMRCA for this node suggests that at least one female from the Southern Hemisphere immigrated to the North Pacific approximately 0.37 Ma. These results provide strong evidence that North Pacific and North Atlantic fin whales should not be considered the same subspecies, and suggest the need for revision of the global taxonomy of the species.

Katarina Topalov, Arndt Schimmelmann, P. David Polly, Peter E. Sauer, and **Mark Lowry**. 2013. Environmental, trophic, and ecological factors influencing bone collagen δ^2 H. Geochimica et Cosmochimica Acta 111:88-104.

Summary Organic deuterium/hydrogen stable isotope ratios (i.e. ${}^{2}H/{}^{1}H$, expressed as $\delta^{2}H$ value in ‰) in animal tissues are related to the ²H/¹H in diet and ingested water. Bone collagen preserves the biochemical 2 H/ 1 H isotopic signal in the δ^2 H value of collagen's non-exchangeable hydrogen. Therefore, δ^2 H preserved in bone collagen has the potential to constrain environmental and trophic conditions, which is of interest to researchers studying of both living and fossil vertebrates. Our data examine the relationship of δ^2 H values of collagen with geographic variation in δ^2 H of meteoric waters, with local variations in the ecology and trophic level of species, and with the transition from mother's milk to adult diet. Based on 97 individuals from 22 marine and terrestrial vertebrates (predominately mammals), we found the relationships of collagen $\delta^2 H$ to both geographic variation in meteoric water δ^2 H (R^2 =0.55) and to δ^{15} N in bone collagen (R^2 =0.17) statistically significant but weaker than previously reported. The second strongest control on collagen $\delta^2 H$ in our data is dietary, with nearly fifty percent of the variance in δ^2 H explained by trophic level (R^2 =0.47). Trophic level effects potentially confound the local meteoric signal if not held constant: herbivores tend to have the lowest δ^2 H values, omnivores have intermediate ones, and carnivores have the highest values. Body size (most likely related to mass-specific metabolic rates) has a strong influence on collagen δ^2 H (R^2 =0.30), by causing greater sensitivity in smaller animals to seasonal climate variations and/or high evapotranspiration leading to ²H-enrichment in tissues. In marine mammals weaning produces a dramatic effect on collagen δ^2 H with adult values being universally higher than pup values (R^2 =0.79). Interestingly, the shift in δ^{15} N at weaning is downward, even though normally hydrogen and nitrogen isotope ratios are positively correlated with one another in respect to trophic level. Our findings suggest that in carnivores, which have an

especially high variance in $\delta^2 H$, large samples are needed to separate signals from precipitation, trophic level, body size, and age. For $\delta^2 H$ of fossil collagen to be useful as a proxy of environmental or dietary information, these confounding effects need to be understood, which means careful selection of a study species. Further, $\delta^2 H$ from a single fossil bone collagen is likely to be uninterpretable.

Week of 13 May 2013

Moore JE, Curtis KA, Lewison RL, Dillingham PW, Cope JM, Fordham SV, Heppell SS, Pardo SA, Simpfendorfer CA, Tuck GN, Zhou S. 2013. Evaluating sustainability of fisheries bycatch mortality for marine megafauna: a review of conservation reference points for data-limited populations. Environmental Conservation (online First View), doi:10.1017/S037689291300012X

Summary - Fisheries by catch threatens populations of marine megafauna such as marine mammals, turtles, seabirds, sharks and rays, but fisheries impacts on non-target populations are often difficult to assess due to factors such as data limitation, poorly defined management objectives and lack of quantitative bycatch reduction targets. Limit reference points can be used to address these issues and thereby facilitate adoption and implementation of mitigation efforts. Reference points based on catch data and life history analysis can identify sustainability limits for bycatch with respect to defined population goals even when data are quite limited. This can expedite assessments for large numbers of species and enable prioritization of management actions based on mitigation urgency and efficacy. This paper reviews limit reference point estimators for marine megafauna bycatch, with the aim of highlighting their utility in fisheries management and promoting best practices for use. Different estimators share a common basic structure that can be flexibly applied to different contexts depending on species life history and available data types. Information on demographic vital rates and abundance is required; of these, abundance is the most data-dependent and thus most limiting factor for application. There are different approaches for handling management risk stemming from uncertainty in reference point and bycatch estimates. Risk tolerance can be incorporated explicitly into the reference point estimator itself, or probability distributions may be used to describe uncertainties in bycatch and reference point estimates, and risk tolerance may guide how those are factored into the management process. Either approach requires simulation-based performance testing such as management strategy evaluation to ensure that management objectives can be achieved. Factoring potential sources of bias into such evaluations is critical. This paper reviews the technical, operational, and political challenges to widespread application of reference points for management of marine megafauna bycatch, while emphasizing the importance of developing assessment frameworks that can facilitate sustainable fishing practices.

TRACEY J. REGAN, **BARBARA L. TAYLOR**, GRANT G. THOMPSON, JEAN FITTS COCHRANE, KATHERINE RALLS, MICHAEL C. RUNGE, AND RICHARD MERRICK. 2013. Testing Decision Rules for Categorizing Species'Extinction Risk to Help Develop Quantitative Listing Criteria for the U.S. Endangered Species Act. Conservation Biology DOI: 10.1111/cobi.12055

Abstract - Lack of guidance for interpreting the definitions of endangered and threatened in the U.S. Endangered Species Act (ESA) has resulted in case-by-case decision making leaving the process vulnerable to being considered arbitrary or capricious. Adopting quantitative decision rules would remedy this but requires the agency to specify the relative urgency concerning extinction events over time, cutoff risk values corresponding to different levels of protection, and the importance given to different types of listing errors. We tested the performance of 3 sets of decision rules that use alternative functions for weighting the relative urgency of future extinction events: a threshold rule set, which uses a decision rule of x% probability of extinction over y years; a concave rule set, where the relative importance of future extinction events declines exponentially over time; and a shoulder rule set that uses a sigmoid shape function, where relative importance declines slowly at first and then more rapidly. We obtained decision cutoffs by interviewing several biologists and then emulated the listing process with simulations that covered a range of extinction risks typical of ESA listing decisions. We evaluated performance of the decision rules under different data quantities and qualities on the basis of the relative importance of misclassification errors. Although there was

little difference between the performance of alternative decision rules for correct listings, the distribution of misclassifications differed depending on the function used. Misclassifications for the threshold and concave listing criteria resulted in more overprotection errors, particularly as uncertainty increased, whereas errors for the shoulder listing criteria were more symmetrical. We developed and tested the framework for quantitative decision rules for listing species under the U.S. ESA. If policy values can be agreed on, use of this framework would improve the implementation of the ESA by increasing transparency and consistency.

Robertson, K. M., Minich, J., **Bowman, A. J**. and **P. A. Morin**. 2013. A thin soup: Extraction and amplification of DNA from DMSO and ethanol used as preservative for cetacean tissue samples. Conservation Genet Resour DOI 10.1007/s12686-013-9934-4.

Summary - Two popular tissue preservatives, 100% ethanol and 20% salt saturated dimethyl sulfoxide (DMSO) solution were tested for the existence of amplifiable, free-floating DNA after 2 to 18 yrs of tissue storage. We found that short mtDNA fragments were consistently amplified and sequenced from DMSO preservative, while nDNA amplification was limited and inconsistent. Amplification of both mtDNA and nDNA failed most of the time for the ethanol samples.

Week of 6 May 2013

BARBARA GALLETTI VERNAZZANI, ELSA CABRERA, and **ROBERT L. BROWNELL, JR.** 2013. Eastern south Pacific southern right whale photo-identification catalog reveals behavior and habitat use patterns. Marine Mammal Science doi:10.1111/mms.12030 (No Abstract)

Jepson PD, Deaville R, et al., incl **R. L. Brownell, Jr**. (2013) What Caused the UK's Largest Common Dolphin (*Delphinus delphis*) Mass Stranding Event? PLoS ONE 8(4): e60953. doi:10.1371/journal.pone.0060953

Abstract - On 9 June 2008, the UK's largest mass stranding event (MSE) of short-beaked common dolphins (Delphinus delphis) occurred in Falmouth Bay, Cornwall. At least 26 dolphins died, and a similar number was refloated/herded back to sea. On necropsy, all dolphins were in good nutritive status with empty stomachs and no evidence of known infectious disease or acute physical injury. Auditory tissues were grossly normal (26/26) but had microscopic haemorrhages (5/5) and mild otitis media (1/5) in the freshest cases. Five lactating adult dolphins, one immature male, and one immature female tested were free of harmful algal toxins and had low chemical pollutant levels. Pathological evidence of mud/seawater inhalation (11/26), local tide cycle, and the relative lack of renal myoglobinuria (26/26) suggested MSE onset on a rising tide between 06:30 and 08:21 hrs (9 June). Potential causes excluded or considered highly unlikely included infectious disease, gas/fat embolism, boat strike, by-catch, predator attack, foraging unusually close to shore, chemical or algal toxin exposure, abnormal weather/climatic conditions, and highintensity acoustic inputs from seismic airgun arrays or natural sources (e.g., earthquakes). International naval exercises did occur in close proximity to the MSE with the most intense part of the exercises (including midfrequency sonars) occurring four days before the MSE and resuming with helicopter exercises on the morning of the MSE. The MSE may therefore have been a "two-stage process" where a group of normally pelagic dolphins entered Falmouth Bay and, after 3-4 days in/around the Bay, a second acoustic/disturbance event occurred causing them to strand en masse. This spatial and temporal association with the MSE, previous associations between naval activities and cetacean MSEs, and an absence of other identifiable factors known to cause cetacean MSEs, indicates naval activity to be the most probable cause of the Falmouth Bay MSE.

Week of 30 April 2013

Jacobson, E. K., T. M. Yack, and J. Barlow. 2013. Evaluation of an automated acoustic beaked whale detection algorithm using multiple validation and assessment methods. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-509, 26 p.

Abstract - Currently, the acoustic detection of beaked whales during passive acoustic surveys requires trained acousticians to identify beaked whale signals with the aid of various software programs. The development of reliable automated detection and classification methods will enable passive acoustic approaches to better meet monitoring needs for real-time mitigation of industry and military impacts. During ongoing development of automated beaked whale detectors and classifiers it will be important for researchers at different institutions to utilize standardized metrics of performance. At the Southwest Fisheries Science Center (SWFSC), automated detection algorithms for Cuvier's beaked whale (Ziphius cavirostris) and Baird's beaked whale (Berardius bairdii) were developed using PAMGUARD software (Douglas Gillespie: www.pamguard.org). To evaluate the performance of these beaked whale detectors, 15 ten-minute recording segments were processed in PAMGUARD, and the resulting signal detections were compared to manual logs of beaked whale signals confirmed by an experienced acoustician. The comparison was conducted using three methods: precise timestamp matching between manual and automated detections, detection counts from one-minute time bins, and binary presence/absence detection classification of one-minute bins. The detections were scored as true positive, false positive, false negative or false classification. Detector efficacy was quantified using measures developed for information retrieval systems (precision, recall, and F-score) as well as the Receiver Operating Characteristic. Calculated performance scores were compared across evaluation methods. We found that the method used to evaluate detector functionality greatly influences the resulting performance scores and subsequently our perception of detector ability. Therefore, it will be important for researchers to clearly communicate methods and results of detector evaluation. To allow for greatest precision and applicability to different recording datasets, we recommend that beaked whale detectors be evaluated using timestamp matching between manual and automated detections in trial datasets and that F-scores be used to compare detectors. This approach avoids problems associated with binning datasets by eliminating the need for a measure of false negatives.

Evans, Jonathan P. and Eric M. **Keen**. 2013. Regeneration Failure in a Remnant Stand of Pignut Hickory (Carya glabra) on a Protected Barrier Island in Georgia, USA. Natural Areas Journal, 33(2):171-176.

Abstract - Maritime forest communities on barrier islands along the Atlantic and Gulf coasts have been severely fragmented by a continuous history of human land use and natural disturbance. Isolated populations of certain tree species in maritime forest fragments may now be too small to be viable and their inability to regenerate may result in their eventual elimination from barrier islands. Using an 11-year study of a population of pignut hickory (Carya glabra), a common species of remnant maritime forest stands on St. Catherine's Island, Georgia, we present a case study of tree regeneration failure on a barrier island. We found that there has been no recruitment of new hickory individuals into the canopy of this population over the last 65 years. Field evidence of browse and a strong correlation between seedling density distributions and microsite protection from herbivory suggest that this trend in recruitment failure is related to an increased abundance of deer (Odocoileus) and pigs (Sus) on the island. Using a size class population projection model, we estimated that, if such recruitment failure and mortality rates continue, the hickory population will be extirpated from the maritime forest within 200 years. Tree species that are failing to regenerate within maritime forests represent a special challenge that is not currently being addressed in the long-term management of barrier island biodiversity.

Week of 16 April 2013

Barlow, J. 2013. Inferring Trackline Detection Probabilities from Differences in Apparent Densities of Beaked Whales and Dwarf & Pygmy Sperm Whales in Different Survey Conditions. NOAA Technical Memorandum, NOAA-TM-508.

Abstract - Visual line-transect surveys are commonly used to estimate the abundance of cetaceans (whales, dolphins, and porpoises). A key parameter in this method is the probability of detecting a cetacean that is directly on the transect line or g(0). Beaked whales and dwarf & pygmy sperm whales are visually inconspicuous and dive for long periods of time. Previous studies have shown that trackline detection probability is low for these species even in the best survey conditions. Trackline detection probability has never been estimated for them in poor survey conditions. A method is developed here to estimate the relative

values of trackline detection probability by comparing estimates of apparent density in different survey conditions (measured as Beaufort state) using estimated density in the best survey conditions as a reference point. Using data from line-transect surveys in the eastern tropical Pacific, this approach yields consistent estimates of trackline detection probability for beaked whales and for dwarf & pygmy sperm whales as functions of sighting conditions in two adjacent study areas. Results show that g(0) for beaked whales is similar for Beaufort 0 and 1 conditions but decreases with increasing Beaufort to less than 10% of that value in Beaufort 5. For dwarf & pygmy sperm whales g(0) decreases even faster with Beaufort state and, in Beaufort 2, is less than 10% of its value in Beaufort 0. These relative values of g(0) are used to extrapolate published estimates of g(0) for calm seas to yield values for Beaufort states 0 to 5.

Week of 8 April 2013

C. S. Baker, A. Hutt, K. Thompson, M. L. Dalebout, J. Robins, **R. L. Brownell Jr**. & G. S. Stone. 2013. Species identity and human consumption of beaked whales in the Gilbert Islands, Republic of Kiribati. Animal Conservation doi:10.1111/acv.12039

Abstract - We investigated the species identity and local use of cetaceans on the Gilbert Islands, Republic of Kiribati. Working with the Kiribati Ministry of Environment, Lands and Agricultural Development and Fisheries Division, we visited the islands of Tarawa, Tabiteuea (North), Butaritari and Onotoa from June to July 2009, and collected 24 bones, bone fragments or teeth attributed to recent strandings. The mitochondrial DNA control region or cytochrome b was successfully amplified from 12 bones or bone fragments and used to identify four species: Mesoplodon sp. representing a new species or subspecies of beaked whale, the dense-beaked whale Mesoplodon densirostris, Cuvier's beaked whale Ziphius cavirostris and the pygmy sperm whale Kogia breviceps. This is the first confirmed identification of the dense-beaked, Cuvier's and pygmy sperm whales from the Gilbert Islands. All specimens were reportedly used for human consumption.

Jone TT, **Seminoff JA.** 2013. Feeding Biology: Advances from Field-Based Observations, Physiological Studies, and Molecular Techniques. In: Musick, J., J. Wyneken, and K. Lohman (Eds.), Biology of the Sea Turtles, Volume 3. CRC Press, Boca Raton, FL. pp. 211-248.

Summary - Since Archie Carr's seminal work in the 1960s and 1970s and efforts by Karen Bjorndal and others in the 1980s and 1990s, feeding biology has been a relatively well-studied facet of sea turtle biology. This is opportune for the science of sea turtles considering that nutrient acquisition strategies are among the most important components of a sea turtle's life history, influencing key demographic parameters such as somatic growth, age-at-maturity, and timing of reproductive migrations. Over the past two decades, however, the advent of new research fields such as physi-ological monitoring, biologging, and stable isotope analysis (SIA) have helped strengthen this understanding even further. These tools have provided insights that have in some cases confirmed earlier wisdom about how a sea turtle makes a living, and in other cases have redefined long- standing biological paradigms. Considering the new information that has come available, it is clear that the ecological strategies of some species are much more diverse than originally considered. For example, green turtles (Chelonia mydas), long-considered obligate neritic herbivores instead eat large amounts of animal matter in many places, and at least in the Pacific are commonly high-seas dwellers, even as adults. Hawksbill turtles (*Eretmochelys imbricata*), the "coral reef dwelling" turtle, are turning up in the strangest of places. In the eastern Pacific, for example, adult hawksbills inhabit mangrove estuaries during non-breeding periods, a huge departure from our belief that the species was tied to coral reefs. In the Caribbean and Indian Ocean, hawksbills are now known to depend on seagrass pastures for foraging and residence. Leatherbacks (Dermochelys coriacea), historically defined as "high-seas inhabitants," are now seen in coastal habitats more than ever before. These and other novel revelations about feeding biology are at least partly due to the globalization of sea turtle research and an everexpanding toolbox at the disposal of field and laboratory scientists. Indeed, more research with both traditional and novel tools is con-ducted in more parts of the world than ever before, and we are now gaining an appreciation of just how complex and adaptive sea turtles can be. Much new biological information has emerged in the published literature since The Biology of the Sea Turtles (Volume 1) was first published and a thorough update is warranted, particularly for aspects relating to feeding biology. In this chapter we present new information for all seven

sea turtle species, building on Karen Bjorndal's chapter on Feeding Biology in Volume 1 that summarized what was known at that time. In Section 9.2 we present the latest information about sea turtle diet and feeding biology. Here we describe new diet items and novel foraging tactics that are reshaping our perceptions about the types of prey consumed and methods by which sea turtles access food resources. In Section 9.3 we focus on the feeding physiology of sea turtles (e.g., specific dynamic action (SDA), digestive efficiency, and passage rates of digesta), a still-understudied area of sea turtle feeding biology, but one that is expanding thanks to additional field and lab-based scientific research. Understanding how sea turtle energy acquisition is constrained by physiological and environmental factors is important as these data factor into growth rates, residency times, population demographics, bioenergetics and energy budgets, and reproductive output. In Sections 9.4 (stable isotopes) and 9.5 (fatty acids and trace elements) we explore the "molecularbased" techniques that are showing great promise for estab- lishing diet, trophic status, and foraging movements of sea turtles. Clearly, the advent of these approaches allows us to learn much about the types of foods consumed by turtles based on the analysis of their own body tissues. As described earlier, the feeding biology of sea turtles is a broad topic with many nuisances. Together the established (e.g., stomach content analysis, esophageal lavage) and emerging (e.g., SIA, fatty acids) techniques give greater insight and understanding into the unique foraging strategies of sea turtles both intra- and interspecifically and through life-history stages. Studies of feeding physiology then begin to tie together what, when, and where sea turtles eat with why and how they eat to meet daily and yearly energy demands of maintenance, growth, and reproduction. In the end, our goal is to provide an update on the current knowledge of sea turtle feeding biology and share a perspective of how our understanding has evolved in the past decades.

MacDonald BD, Madrak SV, Lewison RL, **Seminoff JA**, **Eguchi T.** 2013. Fine scale diel movement of the east Pacific green turtle, *Chelonia mydas*, in a highly urbanized foraging environment. Journal of Experimental Marine Biology and Ecology 443:56–64.

Abstract - Protection of endangered species requires an understanding of their spatial ecology in relation to human activities. Recent improvements in monitoring technologies, such as automated acoustic telemetry, have enabled the collection of these data for mobile marine organisms such as sea turtles. The east Pacific green sea turtle Chelonia mydas uses San Diego Bay, CA, a heavily developed ecosystem, as a year-round foraging ground. We used a combination of manual and automated acoustic telemetry from 2009 to 2011 to elucidate the distribution of green turtles throughout South San Diego Bay and to understand their diel behavior. Tracked turtles (n = 20) ranged in size from 54.9 to 102.5 cm straight carapace length and had fidelity to two sites: the warm-water effluent channel of a waterfront power plant and an eelgrass meadow. Turtles tracked manually during the night were more sedentary (mean swimming speed \pm SE: 0.38 ± 0.03 km h-1) and generally restricted their activity to waters near the power plant. During the day, turtles swam at higher speeds $(0.67 \pm 0.07 \text{ km h} - 1)$ and were mainly found in eelgrass meadows where they are known to forage. Turtles were occasionally found near a shipping terminal, which occurred almost exclusively during the daytime. Turtles in areas of increased boat traffic are at risk of vessel strikes, and future monitoring should investigate the potential for turtle-human interactions in other heavily-used areas of San Diego Bay. Future monitoring should also characterize how turtle behavior may change following the decommissioning of the power plant, which occurred six months before the end of this study.

Week of 1 April 2013

Becker EA, KA Forney, MC Ferguson, **J Barlow**, **JV Redfern**. 2012. Predictive Modeling of Cetacean Densities in the California Current Ecosystem based on Summer/Fall Ship Surveys in 1991- 2008. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-499, 45 p.

Abstract - We use data from six ship-based cetacean and ecosystem assessment surveys in the California Current Ecosystem (CCE) to update habitat-based density models for 11 species and one small-beaked-whale guild. We previously had modeled cetacean density as a function of oceanic variables for the same 12 species/guild using data collected during four line-transect ship surveys conducted in the CCE in summer and fall of 1991, 1993, 1996, and 2001. An independent set of survey data collected in the summer and fall of 2005 was used to validate the models. These estimates were incorporated into a web-based system that allows users to estimate cetacean density within any user-defined region within the CCE study area. In this study, data from an additional line-transect survey conducted in 2008 were pooled with the 1991-2005 data and used to re-build the habitat-based density models. We also refit the 1991-2008 data to the previous "best" models to compare model performance. The additional year of data provided increased sample sizes and a greater range of oceanic conditions for robust model development. Predicted densities for each year were smoothed and then averaged to produce a composite grid that represents our best estimate of CCE cetacean density over the past 20 years. The final model predictions were used to update the web-based system and also provided to the U.S. Navy to help assess potential impacts from their at-sea training and testing activities.

Carretta, J.V., E. Oleson, D.W. Weller, A.R. Lang, K.A. Forney, J. Baker, B. Hanson, K. Martien, M.M. Muto, M.S. Lowry, J. Barlow, D. Lynch, L. Carswell, R. L. Brownell Jr., D. K. Mattila, and M.C. Hill. 2013. U.S. Pacific Marine Mammal Stock Assessments: 2012. U.S. Department of Commerce, NOAA Technical Memorandum, NMFS-SWFSC-504. 378 p.

Available at http://swfsc.noaa.gov/prd-sars/

Frey A, Dutton PH, and Balazs GH (2013) Insights on the demography of cryptic nesting by green turtles (*Chelonia mydas*) in the main Hawaiian Islands from genetic relatedness analysis. Journal of Experimental Marine Biology and Ecology 442: 80–87 http://dx.doi.org/10.1016/j.jembe.2013.01.030

Abstract - Within the Hawaiian archipelago, green turtle nesting has occurred almost exclusively in the northwestern Hawaiian Islands, mainly at French Frigate Shoals (FFS), however an increase in occasional nesting has recently been observed on the main Hawaiian Islands (MHI). Due to logistical constraints, monitoring the nesting activity on the MHI has been limited to nest documentation. Without systematic tagging of the nesting females it is not clear how many are nesting here. We used mitochondrial (mt) DNA sequencing combined with nuclear (n) DNA analysis based on 14 microsatellite markers to infer the number of individual nesters. Genotypes were determined for 181 dead embryos and hatchlings salvaged from 71 nests laid on Maui, Molokai, Kauai, Lanai, and Oahu, along with those of 81 nesting females that were sampled on FFS. MtDNA results showed that 58% of the MHI clutches were laid by females with a relatively rare haplotype only reported in 16% of the FFS nesting population. Nuclear DNA results showed that nesting in the MHI might be attributed to a relatively small number of females that appear to be related to each other. We were able to reconstruct genotypes for nesting females from hatchling profiles and we estimate that 15 different females were responsible for clutches laid on the MHI. Taken together, the mtDNA and nDNA results suggest that the nesting population at the MHI may be the result of a few founders that originated from the FFS breeding population, possibly facilitated by captive rearing and release of FFS juveniles locally from Oahu. We suggest that this regional range expansion may buffer against the loss of current nesting sites at FFS due to sea level rise. Our results demonstrate the potential for genetic tools to be incorporated into population assessment, particularly in areas where access to reproductive females is difficult and population size is unknown.

Ruiz-Cooley, R.I., L.T. Ballance, and M.D. McCarthy. 2013. Range expansion of the jumbo squid in the NE Pacific: δ^{15} N decrypts multiple origins, migration and habitat use. PLoS ONE 8(3):e59651. doi:10.1371/journal/pone.0059651.

Abstract - Coincident with climate shifts and anthropogenic perturbations, the highly voracious jumbo squid Dosidicus gigas reached unprecedented northern latitudes along the NE Pacific margin post 1997–98. The physical or biological drivers of this expansion, as well as its ecological consequences remain unknown. Here, novel analysis from both bulk tissues and individual amino acids (Phenylalanine; Phe and Glutamic acid; Glu) in both gladii and muscle of D. gigas captured in the Northern California Current System (NCCS) documents for the first time multiple geographic origins and migration. Phe δ^{15} N values, a proxy for habitat baseline δ^{15} N values, confirm at least three different geographic origins that were initially detected by highly variable bulk $\delta^{15}N$ values in gladii for squid at small sizes (<30 cm gladii length). In contrast, bulk $\delta^{15}N$ values from gladii of large squid (>60 cm) converged, indicating feeding in a common ecosystem. The strong latitudinal gradient in Phe δ^{15} N values from composite muscle samples further confirmed residency at a point in time for large squid in the NCCS. These results contrast with previous ideas, and indicate that small squid are highly migratory, move into the NCCS from two or more distinct geographic origins, and use this ecosystem mainly for feeding. These results represent the first direct information on the origins, immigration and habitat use of this key "invasive" predator in the NCCS, with wide implications for understanding both the mechanisms of periodic D. gigas population range expansions, and effects on ecosystem trophic structure.

Weller, D.W., Bettridge, S., Brownell, R.L., Jr., Laake, J.L., Moore, J.E., Rosel, P.E., Taylor, B.L and Wade, P.R. 2013. Report of the National Marine Fisheries Service gray whale stock identification workshop. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-507

Summary - A single population stock of gray whales (Eschrichtius robustus), referred to as the eastern North Pacific (ENP) stock, is presently recognized in U.S. waters. New information, however, suggests the possibility of recognizing two additional stocks of gray whales in U.S. waters: the Pacific Coast Feeding Group (PCFG) and the western North Pacific (WNP) stock. To evaluate the currently recognized and potentially emerging characterization of gray whale stock structure, NMFS established a scientific Task Force (TF). The overarching objective of this TF was to provide an objective scientific evaluation of gray whale stock structure as defined under the MMPA and implemented through the NMFS Guidelines for Assessing Marine Mammal Stocks (GAMMS; NMFS 2005). More specifically, the TF was convened to provide advice on the primary question – "Is the PCFG a "population stock" under the MMPA and GAMMS guidelines"? In addition, the TF was asked to provide advice on a question of developing importance – "Is stock" under the MMPA**GAMMS** WNPstock a "population and guidelines"?

Week of 25 March 2013

Redfern, J. V., M. F. McKenna, T. J. Moore, J. Calambokidis, M. L. DeAngelis, E. A. Becker, J. Barlow, K. A. Forney, P. C. Fiedler, and S. J. Chivers. 2013. Assessing the risk of ships striking large whales in marine spatial planning. Conservation Biology 27:292-302.

Abstract - Marine spatial planning provides a comprehensive framework for managing multiple uses of the marine environment and has the potential to minimize environmental impacts and reduce conflicts among users. Spatially explicit assessments of the risks to key marine species from human activities are a requirement of marine spatial planning. We assessed the risk of ships striking humpback (Megaptera novaeangliae), blue (Balaenoptera musculus), and fin (Balaenoptera physalus) whales in alternative shipping routes derived from patterns of shipping traffic off Southern California (U.S.A.). Specifically, we developed whale-habitat models and assumed ship-strike risk for the alternative shipping routes was proportional to the number of whales predicted by the models to occur within each route. This definition of risk assumes all ships travel within a single route. We also calculated risk assuming ships travel via multiple routes. We estimated the potential for conflict between shipping and other uses (military training and fishing) due to

overlap with the routes. We also estimated the overlap between shipping routes and protected areas. The route with the lowest risk for humpback whales had the highest risk for fin whales and vice versa. Risk to both species may be ameliorated by creating a new route south of the northern Channel Islands and spreading traffic between this new route and the existing route in the Santa Barbara Channel. Creating a longer route may reduce the overlap between shipping and other uses by concentrating shipping traffic. Blue whales are distributed more evenly across our study area than humpback and fin whales; thus, risk could not be ameliorated by concentrating shipping traffic in any of the routes we considered. Reducing ship-strike risk for blue whales may be necessary because our estimate of the potential number of strikes suggests that they are likely to exceed allowable levels of anthropogenic impacts established under U.S. laws.

Tiwari, M. 2012. Sea Turtle surveys in the Southern Nicobar Islands: Results of surveys from February-May 1991. Indian Ocean Turtle Newsletter 16: 14-18. NO ABSTRACT

Week of 11 March 2013

Stewart KR, James MC, **Roden S and Dutton PH**. 2013. Assignment tests, telemetry, and tag-recapture data converge to identify natal origins of leatherback turtles, *Dermochelys coriacea*, foraging in Canadian waters. Journal of Animal Ecology DOI: 10.1111/1365-2656.12056.

http://onlinelibrary.wiley.com/journal/10.1111/%28ISSN%291365-2656/earlyview

Summary

- 1. Investigating migratory connectivity between breeding and foraging areas is critical to effective management and conservation of highly mobile marine taxa, particularly threatened, endangered, or economically important species that cross through regional, national and international boundaries.
- 2. The leatherback turtle (*Dermochelys coriacea*, Vandelli 1761) is one such transboundary species that spends time at breeding areas at low latitudes in the northwest Atlantic during spring and summer. From there, they migrate widely throughout the North Atlantic, but many show fidelity to one region off eastern Canada, where critical foraging habitat has been proposed. Our goal was to identify nesting beach origins for turtles foraging here.
- 3. Using genetics, we identified natal beaches for 288 turtles that were live-captured off the coast of Nova Scotia, Canada. Turtles were sampled (skin or blood) and genotyped using 17 polymorphic microsatellite markers. Results from three assignment testing programs (ONCOR, GeneClass2 and Structure) were compared. Our nesting population reference data set included 1417 individuals from nine Atlantic nesting assemblages. A supplementary data set for 83 foraging turtles traced to nesting beaches using flipper tags and/or PIT tags (n = 72), or inferred from satellite telemetry (n = 11), enabled ground-truthing of the assignments.
- 4. We first assigned turtles using only genetic information and then used the supplementary recapture information to verify assignments. ONCOR performed best, assigning 64 of the 83 recaptured turtles to natal beaches (77_1%). Turtles assigned to Trinidad (164), French Guiana (72), Costa Rica (44), St. Croix (7), and Florida (1) reflect the relative size of those nesting populations, although none of the turtles were assigned to four other potential source nesting assemblages.
- 5. Our results demonstrate the utility of genetic approaches for determining source populations of foraging marine animals and include the first identification of natal rookeries of male leatherbacks, identified through satellite telemetry and verified with genetics. This work highlights the importance of long-term monitoring and tagging programmes in nesting and highuse foraging areas. Moreover, it provides a scientific basis for evaluating stock-specific effects of fisheries on migratory marine species, thus identifying where coordinated international recovery efforts may be most effective.

Week of 3 March 2013

Kathleen E. Hunt, Michael J. Moore, Rosalind M. Rolland, **Nicholas M. Kellar**, Ailsa J. Hall, Joanna Kershaw, Stephen A. Raverty, Cristina E. Davis, Laura C. Yeates, Teresa K. Rowles, and Scott D. Kraus. *In Review*. Opening

the biggest black box: New approaches to the study of conservation physiology of large whales. Conservation Physiology.

Abstract- Large whales are subjected to a variety of conservation pressures that could be better monitored and managed if physiological information could be gathered readily from free-swimming whales. However, traditional approaches to studying physiology have been impractical for large whales, since there is no routine method for capture of the largest species and there is presently no practical method of obtaining blood samples from free-swimming whales. We review novel techniques for gathering physiological information on large whales using a variety of nonlethal and minimally invasive (or noninvasive) sample matrices. We focus on methods that should produce information relevant to conservation physiology, e.g. measures relevant to stress physiology, reproductive status, nutritional status, immune response, health, and disease. Four types of samples are discussed: fecal samples, respiratory samples ("blow"), skin/blubber samples, and photographic imaging. Fecal samples have historically been used for diet analysis but increasingly are also used for hormonal analyses, as well as for assessment of exposure to toxins, pollutants, and parasites. Blow samples contain many hormones as well as respiratory microbes, metabolites, and a variety of immune-related measures. Biopsy dart samples are widely used for genetic and contaminant analyses and are now being used for endocrine studies along with proteomic and transcriptomic approaches. Photographic analyses have benefited from recently developed quantitative techniques allowing assessment of skin condition, ectoparasite load, and nutritional status, along with wounds and scars from ship strike and fishing gear entanglement. Field application of these novel techniques has the potential to greatly improve our understanding of the physiology of large whales, better enabling assessment of the relative impacts of many anthropgenic and ecological pressures.

Week of 25 February 2013

Peter H. Dutton, Suzanne Roden, Kelly R. Stewart, Erin LaCasella, Manjula Tiwari, Angela Formia, Joao Carlos Thomé, Suzanne R. Livingstone, Scott Eckert, Didiher Chacon-Chaverri, Philippe Rivalan, Phil Allman. Population stock structure of leatherback turtles (*Dermochelys coriacea*) in the Atlantic revealed using mtDNA and microsatellite markers. Conservation Genetics DOI 10.1007/s10592-013-0456-0.

Abstract - This study presents a comprehensive genetic analysis of stock structure for leatherback turtles (Dermochelys coriacea), combining 17 microsatellite loci and 763 bp of the mtDNA control region. Recently discovered eastern Atlantic nesting populations of this critically endangered species were absent in a previous survey that found little ocean-wide mtDNA variation. We added rookeries in West Africa and Brazil and generated longer sequences for previously analyzed samples. A total of 1,417 individuals were sampled from 9 nesting sites in the Atlantic and SW Indian Ocean. We detected additional mtDNA variation with the longer sequences, identifying ten polymorphic sites that resolved a total of ten haplotypes, including three new variants of haplotypes previously described by shorter sequences. Population differentiation was substantial between all but two adjacent rookery pairs, and F_{ST} values ranged from 0.034 to 0.676 and 0.004 to 0.205 for mtDNA and microsatellite data respectively, suggesting that male-mediated gene flow is not as widespread as previously assumed. We detected weak ($F_{ST} = 0.008$ and 0.006) but significant differentiation with microsatellites between the two population pairs that were indistinguishable with mtDNA data. POWSIM analysis showed that our mtDNA marker had very low statistical power to detect weak structure (F_{ST} < 0.005), while our microsatellite marker array had high power. We conclude that the weak differentiation detected with microsatellites reflects a fine scale level of demographic independence that warrants recognition, and that all 9 of the nesting colonies should be considered as Demographically Independent Populations (DIPs) for conservation. Our findings illustrate the importance of evaluating the power of specific genetic markers to detect structure in order to correctly identify the appropriate population units to conserve.

Koch V, Peckham H, Mancini A, **Eguchi T.** 2013. Estimating At-Sea Mortality of Marine Turtles from Stranding Frequencies and Drifter Experiments. PLoS ONE 8(2): e56776. doi:10.1371/journal.pone.0056776

Abstract - Strandings of marine megafauna can provide valuable information on cause of death at sea. However, as stranding probabilities are usually very low and highly variable in space and time, interpreting the results can be challenging. We evaluated the magnitude and distribution of at-sea mortality of marine turtles along the Pacific coast of Baja California Sur, Mexico during 2010-11, using a combination of counting stranded animals and drifter experiments. A total of 594 carcasses were found during the study period, with loggerhead (62%) and green turtles (31%) being the most common species, 87% of the strandings occurred in the southern Gulf of Ulloa, a known hotspot of loggerhead distribution in the Eastern Pacific. While only 1.8% of the deaths could be definitively attributed to bycatch (net marks, hooks), seasonal variation in stranding frequencies closely corresponded to the main fishing seasons. Estimated stranding probabilities from drifter experiments varied among sites and trials (0.05–0.8), implying that only a fraction of dead sea turtles can be observed at beaches. Total mortality estimates for 15-day periods around the floater trials were highest for PSL, a beach in the southern Gulf of Ulloa, ranging between 11 sea turtles in October 2011 to 107 in August 2010. Loggerhead turtles were the most numerous, followed by green and olive ridley turtles. Our study showed that drifter trials combined with beach monitoring can provide estimates for death at sea to measure the impact of small-scale fisheries that are notoriously difficult to monitor for by-catch. We also provided recommendations to improve the precision of the mortality estimates for future studies and highlight the importance of estimating impacts of small- scale fisheries on marine megafauna.

Week of 18 February 2013

Jelh, Jr., J. R. and **A. E. Henry**. Intra-organ flexibility in the eared grebe *Podiceps nigricollis* stomach: a spandrel in the belly. Journal of Avian Biology 44: 001–005, 2013doi: 10.1111/j.1600-048X.2012.00059.x

Abstract - Adjustments in body composition over the annual cycle have been documented in many organs and muscle groups. Here we consider the nature and significance of intra-organ variation in the eared grebe Podiceps nigricollis stomach, a large and variable organ that can weigh 30 g when birds are staging, drop to 8–11 g before setting off, or to as little as 6.6 g after a several-day migration. Weight reduction in association with migration is conventionally regarded as an adaptation to reduce wing loading and flight costs. This interpretation applies to the premigratory reduction of the entire stomach. However, it does not fit the differential in-flight reduction of the proventriculus, because grebes require a large proventriculus to initiate digestion, and its smaller size when they need to rebuild the entire stomach and resume feeding quickly is opposite that expected in a functional context. We view the reduction of the proventriculus as a non-adaptive response, or spandrel, stemming from its intrinsically higher turnover rate. Starving birds, like migrants, also need to digest food quickly. In their case, the proventriculus is maintained as body weight declines and the gizzard is sacrificed. Mechanisms by which individual organisms achieve different responses to similar challenges, including starvation, merit further investigation.

Week of 11 February 2013

Becker, E. A., K. A. Forney, D. G. Foley, and **J. Barlow**. 2012. Density and spatial distribution patterns of cetaceans in the central North Pacific based on habitat models. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-490, 34 p.

Abstract - Habitat-based density models were developed for cetaceans in the Central North Pacific based on cetacean survey data collected by the Southwest Fisheries Science Center in 1997-2006. Cetacean sighting data were collected on systematic line-transect surveys in the temperate eastern Pacific, around Hawaii and other Pacific Islands, and in the eastern tropical Pacific west of 120 degrees longitude. Habitat variables, derived from satellite data, included sea surface temperature, sea surface chlorophyll, sea surface height root-mean-square, primary productivity, distance to land, latitude, and longitude. Models were developed for the pantropical spotted dolphin, spinner dolphin, striped dolphin, rough-toothed dolphin, common bottlenose dolphin, false killer whale, short-finned pilot whale, sperm whale, Bryde's whale, and an "other dolphins"

group that included the short-beaked common and Pacific white-sided dolphin. Uniform densities were estimated for species/guilds that had insufficient sightings for modeling, including pygmy killer whale, Risso's dolphin, killer whale, a small beaked whale guild (including Cuvier's beaked whale and beaked whales of the genus *Mesoplodon*), and pygmy/dwarf sperm whale. Although validation using an independent survey was not possible, modeled density estimates for the 10 species/species group were compared to previously published line-transect density estimates derived within the U.S. Exclusive Economic Zone around Hawaii. The model-based estimates of abundance fall within the 95% confidence limits of the standard line-transect analyses, and they provide greater spatial resolution of the density estimates based on habitat associations. These new models are intended as baseline density estimates for Navy planning and environmental impact statements, to be updated and improved as additional survey data become available in the future.

Moore, J., and D. Weller. 2013. Probability of taking a western gray whale during the proposed Makah hunt. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-507, 13 p.

Executive Summary - Recent observations of gray whales (Eschrichtius robustus) identified in the western North Pacific (WNP) migrating to areas off the coast of North America (Alaska to Mexico) raise concern about the possibility of the small western population being subjected to the gray whale hunt proposed by the Makah Indian Tribe in northern Washington, USA. To address this concern, we estimated the probability of striking (i.e. killing or seriously injuring) a WNP whale during the Makah hunt using six models from 4 model sets that varied based on the assumptions and types of data used for estimation. Model set 1 used WNP and ENP abundance estimates. Model set 2 used these abundance estimates, as well as sightings data from the proposed hunt area. Model sets 3 and 4 used only the sightings data. Within model sets 1 and 2, two models (A and B) differed based upon whether migrating ENP and WNP whales were assumed to be equally available to the hunt per capita (A) or whether this assumption is relaxed (B). We consider Model 2B the most plausible of all models because model set 2 makes use of all available information and 2B contains fewer assumptions than 2A. Based on model 2B, the probability of striking ≥1 WNP whale in a single season ranges from 0.007 to 0.036, depending on if the median or upper 95th percentile estimate is used and on which maximum is used for the total number of whales struck. The probability of striking >1 WNP whale out of 5 seasons ranges from 0.036 to 0.170 across the same scenarios. The expected number to be struck in a single year ranges from 0.01 to 0.04 and from 0.04 to 0.19 across 5 years. For context, these strike estimates were compared to different possible values of Potential Biological Removal (PBR). We also summarized analogous estimates for the number of WNP whales that would be "taken" non-lethally, in terms of the number of attempted but unsuccessful strikes as well as the number of animals approached and pursued during the hunt.

Week of 4 February 2013

Curry, BE, K.Ralls, **R.L. Brownell Jr**. 2013. Prospects for captive breeding of poorly known small cetacean species. Endangered Species Research 19:223-243.

Abstract - Because of the precarious condition of small cetacean species and subpopulations listed as Endangered or Critically Endangered by the IUCN, use of captive breeding for conservation has been suggested for some of them, and will likely be suggested for others. A successful captive breeding program for a new species cannot be implemented until reliable capture and husbandry techniques have been developed. Techniques for assisted reproduction and reintroduction may also be needed. We review attempts to capture, maintain, and breed poorly known small cetaceans and discuss assisted reproductive technologies (ART) that have been used to enhance captive breeding efforts for other small cetaceans. We conclude that the techniques required for successful captive breeding of most Endangered or Critically Endangered small cetacean species have not been sufficiently developed. Development of these techniques should begin before a species or population is Critically Endangered. In particular, ARTs tend to be species specific, necessitating considerable time, money, and research to develop for each species of concern. Critically Endangered populations cannot afford to lose the individuals needed for technique development. The fairly large captive

population sizes necessary (to avoid loss of genetic diversity, inbreeding, and genetic adaptation to captivity), limited space available in aquariums, and high costs of captive breeding and reintroduction programs make it unlikely that captive breeding will play a major role in the conservation of most small cetaceans. The substantive conservation measures needed to prevent extinction of Critically Endangered small cetaceans is reduction or elimination of their primary threats, which are usually by-catch and habitat loss.

Fiedler, P. C., R. Mendelssohn, D. M. Palacios, and S. J. Bograd. 2013. Pycnocline variations in the eastern tropical and North Pacific, 1958–2008. J. Climate 26:583–599.

Abstract - Climatic variability of the pycnocline in the eastern tropical and North Pacific has oceanographic and ecological implications. Gridded monthly profiles of temperature and salinity from the Simple Ocean Data Assimilation (SODA) reanalysis, 1958–2008, were used to derive estimates of four variables related to the density structure of the upper-ocean water column: surface temperature, pycnocline depth, mixed layer depth, and stratification (potential energy anomaly). The pycnocline is primarily a thermal gradient in this region, except in subarctic waters at the northern extreme of the study area, where salinity becomes more important than temperature in determining stratification. Spatial patterns of mean and standard deviation of the four pycnocline variables are presented. Partitioning of variance between seasonal and interannual scales shows the predominance of interannual variability in the tropics and seasonal variability at higher latitudes. Low-frequency variations (trends) in the pycnocline variables were derived by state-space analysis of time series averaged in 5° squares. Regionally coherent trends were either monotonic over 50 years or had decadal-scale changes in sign (±5-10-m depth, ±5%-10% of stratification). For example, in the eastern equatorial Pacific, the pycnocline shoaled by 10 m and weakened by 5% over the 50 years, while in the California Current the pycnocline deepened by ~5 m but showed little net change in stratification, which weakened by 5% to the mid-1970s, strengthened by 8% to the mid-1990s, and then weakened by 4% to 2008. These observed changes in the pycnocline, and future changes resulting from global climate change, may have important biological and ecosystem effects.

Hancock-Hanser, B.L., A. Frey, M.S. Leslie, P.H. Dutton, F.I. Archer, and P.A. Morin. 2013. Targeted multiplex next-generation sequencing: advances in techniques of mitochondrial and nuclear DNA sequencing for population genomics. Molecular Ecology Resources doi: 10.1111/1755-0998.12059

Abstract - Next-generation sequencing (NGS) is emerging as an efficient and cost-effective tool in population genomic analyses of nonmodel organisms, allowing simultaneous resequencing of many regions of multi-genomic DNA from multiplexed samples. Here, we detail our synthesis of protocols for targeted resequencing of mitochondrial and nuclear loci by generating indexed genomic libraries for multiplexing up to 100 individuals in a single sequencing pool, and then enriching the pooled library using custom DNA capture arrays. Our use of DNA sequence from one species to capture and enrich the sequencing libraries of another species (i.e. cross-species DNA capture) indicates that efficient enrichment occurs when sequences are up to about 12% divergent, allowing us to take advantage of genomic information in one species to sequence orthologous regions in related species. In addition to a complete mitochondrial genome on each array, we have included between 43 and 118 nuclear loci for low-coverage sequencing of between 18 kb and 87 kb of DNA sequence per individual for single nucleotide polymorphisms discovery from 50 to 100 individuals in a single sequencing lane. Using this method, we have generated a total of over 500 whole mitochondrial genomes from seven cetacean species and green sea turtles. The greater variation detected in mitogenomes relative to short mtDNA sequences is helping to resolve genetic structure ranging from geographic to species-level differences. These NGS and analysis techniques have allowed for simultaneous population genomic studies of mtDNA and nDNA with greater genomic coverage and phylogeographic resolution than has previously been possible in marine mammals and turtles.

Week of 28 January 2013

Pitman, R. L. 2013. Clipperton Island. Pp. 471-473, *in* Robert Warren Howarth (ed.), Biomes and Ecosystems: An Encyclopedia. Salem Press, Ipswich, MA.

Week of 22 January 2013

X. Zhao, D. Wang, S. T. Turvey, **B. Taylor** and T. Akamatsu. Distribution patterns of Yangtze finless porpoises in the Yangtze River: implications for reserve management. Animal Conservation doi:10.1111/acv.12019

Abstract - The Yangtze finless porpoise (Neophocaena asiaeorientalis asiaeorientalis) is a highly threatened cetacean endemic to the middle and lower reaches of the Yangtze River that has suffered a dramatic decline in recent decades. We characterize and quantify recent distribution patterns of porpoises in the Yangtze River in order to facilitate strategic management of existing in situ cetacean reserves and maximize effective utilization of limited conservation resources. We calculated porpoise relative abundance (encounter rate) using a 1-km moving average along the Yangtze main stem based on a combined visual and acoustic survey conducted in 2006. We then evaluated conservation priority areas based on encounter rates along the river. High-porpoise density areas (> 0.20 porpoises km-1) cover approximately one-third (33.9%, 599 km) of the survey area and contain approximately two-thirds of the porpoise population, making them priority areas for porpoise conservation. In contrast, low-porpoise density areas (0.05 porpoises km-1) cover 28.8% (509 km) of the survey area but contain only 4.5% of the porpoise population, and may already be of little value for porpoise conservation. Five high-priority porpoise conservation sites and five sections that now contain few or no surviving porpoises are identified. Proposed spatial modifications to existing reserves and associated conservation recommendations are made for five existing protected areas along the Yangtze main stem, and we emphasize that some additional river sections should urgently be designated as new protected areas given their high porpoise density. Our approach for identifying conservation priorities may provide lessons for reserve design and management in other protected area networks.

Week of 14 January 2013

Allen CD, Lemons GE, Eguchi T, LeRoux RA, Fahy CC, Dutton PH, Peckham SH, Seminoff JA. 2013. Stable isotope analysis reveals migratory origin of loggerhead turtles in the Southern California Bight. Marine Ecology Progress Series 472: 275–285.

Abstract - Loggerhead turtles Caretta caretta in the North Pacific are listed as Endangered under the US Endangered Species Act and the IUCN Red List. Due partly to their imperiled status, the US National Marine Fisheries Service established a time-area closure in 2003 for the California drift gillnet (CDGN) fishery operating within the Southern California Bight (SCB) to avoid incidental captures. This closure is triggered when sea surface temperatures are above normal, generally caused by El Niño-derived warm-water conditions, which is the time when loggerheads are thought to enter the SCB. Knowledge of the previous foraging grounds of loggerheads incidentally captured by the CDGN fishery in the SCB will help elucidate the oceanographic mechanisms that may influence turtle movement into this region and can assist in optimizing the environmental triggers for implementation of the SCB fishing closure. Stable carbon (δ 13C) and nitrogen (δ15N) isotope analysis was used to determine the previous foraging grounds of logger- heads encountered in the SCB. Skin samples from loggerheads captured in the CDGN fishery were compared with skin from loggerheads in the central North Pacific, incidentally caught in the Hawaii-based longline fishery, as well as skin from turtles sampled during in-water research along the Baja California Peninsula, Mexico. The stable isotope values of CDGN-caught turtles were more similar to those from the central North Pacific than to those from Baja, indicating movements from the central North Pacific to the SCB. We elaborate on potential oceanographic mechanisms by which turtles access the SCB and provide insights that can inform future management decisions for the time-area closure.

Curtis KA, **Moore JE**. 2013. Calculating reference points for anthropogenic mortality of marine turtles. Aquatic Conservtion: Marine and Freshwater Ecosystems. DOI:10.1002/aqc.2308 http://onlinelibrary.wiley.com/doi/10.1002/aqc.2308/abstract

Abstract - 1. Human-caused mortality threatens many marine turtle populations worldwide, with fisheries interactions being a primary cause for population declines. National and international management of fisheries interactions with marine turtles are rarely tied to turtle population biology. Quantitative tools tied to population-based objectives can provide insight into the effectiveness and urgency of bycatch mitigation. 2. A management approach is proposed based on a bycatch control rule called Reproductive Value Loss Limit (RVLL), generalized from the Potential Biological Removal management model for marine mammal populations. For RVLL, population size is scaled by reproductive value to account for strongly agestructured population dynamics and age-dependent fisheries mortality rates in marine turtle populations. 3. RVLL is an estimate of maximum sustainable mortality for a population, calculated from estimates of maximum population growth rate, total reproductive value in the population, and an uncertainty factor. RVLL estimates correspond to specified management goals and risk tolerances. For demonstration, simultaneous goals of maintaining populations above the maximum net productivity level (analogous to the population size that produces maximum sustainable yield) and preventing a decrease in adults are assumed, both with 95% probability. A management-strategy-evaluation-like process was used to explore parameterization of the RVLL equation for robust performance over a range of plausible life history characteristics and uncertainties in abundance and bycatch mortality estimates for marine turtle populations. 4. The RVLL-based management approach presented here proved robust to several important sources of uncertainty and to violation of several key underlying assumptions, and can be adapted to account for important sources of bias. The architecture presented, including tailored management strategy evaluation, provides a useful basis for further development of reference-point-based management of human-added mortality in populations that experience large changes with age in reproductive value and human-caused mortality rates, as is the case for marine turtles.

Week of 7 January 2013

Staaf, D.J., **J.V. Redfern**, W.F. Gilly, W. Watson, and **L.T. Ballance**. 2013. Distribution of ommastrephid paralarvae in the eastern tropical Pacific. Fishery Bulletin 111:78-89.

Abstract—Jumbo squid (Dosidicus gigas) and purpleback squid (Sthenoteuthis oualaniensis) (Teuthida: Ommastrephidae) are thought to spawn in the eastern tropical Pacific. We used 10 years of plankton tow and oceanographic data collected in this region to examine the reproductive habits of these 2 ecologically important squid. Paralarvae of jumbo squid and purpleback squid were found in 781 of 1438 plankton samples from surface and oblique tows conducted by the Southwest Fisheries Science Center (NOAA) in the eastern tropical Pacific over the 8-year period of 1998–2006. Paralarvae were far more abundant in surface tows (maximum: 1588 individuals) than in oblique tows (maximum: 64 individuals). A generalized linear model analysis revealed sea-surface temperature as the strongest environmental predictor of paralarval presence in both surface and oblique tows; the likelihood of paralarval presence increases with increasing temperature. We used molecular techniques to identify paralarvae from 37 oblique tows to species level and found that the purpleback squid was more abundant than the jumbo squid (81 versus 16 individuals).

Turvey ST, Risly CL, **Moore JE**, Barrett LA, Yujiang H, Xiujiang Z, Kaiya Z, Ding W. 2013. Can local ecological knowledge be used to assess status and extinction drivers in a threatened freshwater cetacean? Biological Conservation 157:352-360.

Abstract - Local ecological knowledge constitutes a potentially useful source of information for conservation, but the quality, limitations and biases of this body of knowledge remain largely untested. The Yangtze finless porpoise (*Neophocaena asiaeorientalis asiaeorientalis*) is a highly threatened freshwater cetacean found in one of the world's most densely populated human environments. The dynamics of porpoise decline remain poorly understood, and local ecological knowledge from fishing communities across its range may represent an important conservation tool for monitoring porpoise population status and quantifying levels of human-caused mortality. We used interview data from an extensive survey of fishing communities across the middle-lower Yangtze drainage to investigate spatial and temporal patterns of

porpoise abundance, mortality and population change. Interview data on porpoise relative abundance and decline, especially weekly sighting frequencies, show congruent spatial patterns with data collected from boat-based Yangtze cetacean surveys, demonstrating that informant data can provide accurate quantitative information on these two key parameters of species conservation status. Interview-based collection of local ecological knowledge therefore represents a useful monitoring method for assessing population trends in freshwater cetaceans and other charismatic or distinctive aquatic species, and may be particularly appropriate in regions where resources for regular boat-based surveys are limited. Using local ecological knowledge to identify primary threats to the porpoise population is less straightforward due to probable biases in interview data on porpoise mortality. However, interview data are able to demonstrate that the number of porpoises killed annually in the Yangtze mainstem may have doubled, and that annually mortality rate may have quadrupled, over the past two decades, with mortality due to vessel strikes and other factors having increased more in recent years than by-catch mortality. It seems unlikely that fisheries mortality has been the dominant driver of porpoise decline in the Yangtze mainstem, suggesting that regulating regional fisheries may not be sufficient for porpoise conservation.